

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 106.251 Seconds  
(without alignments)

487.964 Million cell updates/sec

Title: US-10-700-632-7

Perfect score: 622

Sequence: 1 QVQLQPGAEVVKPGASVKM.....EVRLRYFDVWGAGTIVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	622	100.0	118	ADO32091	Ado32091 Mouse ant
2	618	99.4	117	ADO32157	Ado32157 Mouse ant
3	613	98.6	118	ADO32093	Ado32093 Humanised
4	536.5	86.3	121	ADJ94605	Adj94605 Chimeric
5	536.5	86.3	121	ADJ94607	Adj94607 Chimeric
6	534.5	85.9	140	AAR55215	Aar55215 Murine va
7	534.5	85.9	412	AAB30694	Aab30694 A fusion
8	534.5	85.9	412	ABJ39009	Abj39009 B9E9 scFv
9	533.5	85.8	140	ABR55873	AbR55873 Anti-CD20
10	533.5	85.8	140	ABU08394	Abu08394 Murine an
11	533.5	85.8	140	ADC66270	Ade66270 Mouse ant
12	533.5	85.8	140	ADCE8590	Ade85690 Murine im
13	533.5	85.8	140	ADE73084	Ade73084 Murine FU
14	533.5	85.8	140	ADF60661	Adf60661 Protein r
15	533.5	85.8	140	ADN49734	Adn49734 Mature va
16	533.5	85.8	140	ADU74410	Adu74410 Mouse ant
17	533.5	85.8	140	ADV92492	Adv92492 2B8 heavy
18	533.5	85.8	140	ADV98555	Adv98555 Novel chi
19	533.5	85.8	140	ADZ59909	Adz59909 Glycoprot
20	533.5	85.8	360	AAE27924	Aae27924 Human CH2
21	533.5	85.8	360	ABB82833	Abb82833 Antibody
22	533.5	85.8	368	ADW77074	Adw77074 Heavy cha
23	533.5	85.8	451	ADL92472	Adl92472 Antibody
24	533.5	85.8	451	ADL92473	Adl92473 Improved

#### ALIGNMENTS

##### RESULT 1

ADO32091

ID ADO32091 standard; protein; 118 AA.

XX AC ADO32091;

XX AC ADO32091;

DT 12-AUG-2004 (first entry)

DE Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.

XX anti-CD33 antibody; epitope-binding fragment;

KW complementarity-determining region; CDR; immunconjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;

KW heavy chain.

XX Mus musculus.

XX WO2004043344-A2.

XX 27-MAY-2004.

PF 05-NOV-2003; 2003WO-US032737.

PR 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

XX Hoffee MG, Tavares D, Lutz RJ;

DR WPI: 2004-411619/38.

DR N-PSDB; ADO32140.

PT New antibodies that bind to CD33, useful for treating a disease associated with CD33 expression, such as myelodysplastic syndrome, acute or chronic myeloid leukemia.

XX Claim 5; SEQ ID NO 7; 124pp; English.

PS The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunconjugate comprising the antibody or its epitope-binding fragment linked to a drug or prodrug; (2) a composition comprising the antibody or epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical

composition comprising the immunoconjugate, composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the growth of a cell expressing CD33 by contacting the cell with the above defined antibody or its epitope-binding fragment, immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polynucleotide encoding the antibody or its epitope-binding fragment defined above; (9) an isolated polynucleotide encoding a light or heavy chain of the antibody defined above or its epitope-binding fragment; (10) a recombinant vector comprising the polynucleotide; (11) a host cell transformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) obtaining CD33 from a biological material. The anti-CD33 antibody has cytostatic activity. The antibody or its epitope-binding fragment, immunoconjugate, composition can be used for treating a subject having a disease where CD33 is expressed, such as myelodysplastic syndrome, acute myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia. It can also be used for inhibiting the growth of cells expressing CD33, and for in vivo imaging or as affinity purification agents. The present sequence represents the mouse anti-CD33 antibody My9-6 heavy chain variable region, which is used in an example from the present invention.

Sequence 118 AA:

Query Match	100.0%;	Score 622;	DB 8;	Length 118;
Best Local Similarity	100.0%;	Pred. No. 2.6e-45;		
Matches 118;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
1	QVQLQOPGAEVVKPGASVVMSCKASGYTFTSYIIHWIKITQPGGLEWGVVTPGNDDISY	60		
1	QVQLQOPGAEVVKPGASVVMSCKASGYTFTSYIIHWIKITQPGGLEWGVVTPGNDDISY	60		
61	NQKPFKGKATLTADKSTTAYMOLSSLTSDSNAVYTCAREVRLRYFDVWCAGTTVTVSS	118		
61	NQKPFKGKATLTADKSTTAYMOLSSLTSDSNAVYTCAREVRLRYFDVWCAGTTVTVSS	118		

RESULT 2	
DO032157	
D	ADO32157 standard; protein; 117 AA.
C	
C	ADO32157;
T	
K	12-AUG-2004 (first entry)
K	
K	Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73.
E	
K	anti-CD33 antibody; epitope-binding fragment;
K	complementarity-determining region; CDR; immunoconjugate; cytostatic;
W	antibody; myelodysplastic syndrome; acute myeloid leukaemia;
W	chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.
W	
K	
K	Mus musculus.
S	
K	WO2004043344-A2.
N	
N	
K	
D	27-MAY-2004.
K	
K	05-NOV-2003; 2003WO-US032737.
F	
K	
K	07-NOV-2002; 2002US-0424332P.
R	
R	
K	(IMMU-) IMMUNOGEN INC.
A	
A	
K	
I	Hoffee MG, Tavares D, Lutz RJ;
K	
K	WPI; 2004-411619/38.
R	
K	
X	New antibodies that bind to CD33, useful for treating a disease
T	associated with CD33 expression, such as myelodysplastic syndrome, acute
T	myeloid leukemia, and acute myeloid leukemia.

or chronic myeloid leukemia.

Example 3; SEQ ID NO 73; 124pp; English.

The present invention describes an isolated anti-CD33 antibody or its epitope-binding fragment comprising: (a) at least one complementarity-determining region (CDR); or (b) at least heavy chain variable region comprising 3 CDRs, and at least one light chain variable region, where the CDR has the ability to bind CD33. Also described: (1) an immunoconjugate comprising the antibody or its epitope-binding fragment linked to a drug or prodrug; (2) a composition comprising the antibody or epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical composition comprising the immunoconjugate, composition or the antibody defined above, or its epitope-binding fragment, and a pharmaceutical agent; (4) a diagnostic reagent comprising the antibody defined above, where the antibody or antibody fragment is labelled; (5) inhibiting the growth of a cell expressing CD33 by contacting the cell with the above defined antibody or its epitope-binding fragment, immunoconjugate, or (pharmaceutical) composition; (6) determining whether a biological sample contains a myelogenous cancer cell; (7) an improved antibody or its epitope-binding fragment that specifically binds to CD33; (8) an isolated polynucleotide encoding the antibody or its epitope-binding fragment defined above; (9) an isolated polynucleotide encoding a light or heavy chain of the antibody defined above or its epitope-binding fragment; (10) a recombinant vector comprising the polynucleotide; (11) a host cell transformed with the recombinant vector; (12) producing an antibody or its epitope-binding fragment having the ability to bind CD33; and (13) obtaining CD33 from a biological material. The anti-CD33 antibody has cytostatic activity. The antibody or its epitope-binding fragment, immunoconjugate, composition can be used for treating a subject having a disease where CD33 is expressed, such as myelodysplastic syndrome, acute myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia. It can also be used for inhibiting the growth of cells expressing CD33, and for in vivo imaging or as affinity purification agents. The present sequence represents a mouse anti-CD33 antibody heavy chain homologous amino acid sequence, which is used in an example from the present invention.

Sequence 117 AA;

Query Match 99.4%; Score 618; DB 8; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.6e-45;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVWVPGASVKMSCKASGYTFTSYIHNIKQTGGGLEWGVYFGNDDISY 60  
DB 1 QVQLQPGAEVWVPGASVKMSCKASGYTFTSYIHNIKQTGGGLEWGVYFGNDDISY 60

QY 61 NQKFKGKATLTADKSSTTAYMQLSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVS 117  
DB 61 NQKFKGKATLTADKSSTTAYMQLSLTSEDSAVYYCAREVRLRYFDVWGAGTTVTVS 117

RESULT 3  
AD032093  
ID ID  
XN ADO32093 standard; protein; 118 AA.  
AC ADO32093;  
XX  
XX  
12-AUG-2004 (first entry)  
DT DT  
DE DE  
DE Humanised mouse anti-CD33 antibody My9-6 heavy chain SEQ ID NO:9.  
XX  
KW anti-CD33 antibody; epitope-binding fragment;  
KW complementarity-determining region; CDR; immunoconjugate; cytostatic;  
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;  
KW My9-6; heavy chain.  
XX  
XX Mus musculus.  
OS  
OS Homo sapiens.  
OS Synthetic.  
XX

PN WO2004043344-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 PF 05-NOV-2003; 2003WO-US032737.  
 XX  
 PR 07-NOV-2002; 2002US-0424332P.  
 XX  
 PA (IMMU-) IMMUNOGEN INC.  
 XX  
 XX Hoffee MG, Tavares D, Lutz RJ;  
 PI WPI; 2004-411619/38.  
 XX  
 DR  
 XX  
 PT New antibodies that bind to CD33, useful for treating a disease  
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute  
 PT or chronic myeloid leukemia.  
 XX  
 PS Claim 11; SEQ ID NO 9; 124pp; English.  
 XX  
 CC The present invention describes an isolated anti-CD33 antibody or its  
 CC epitope-binding fragment comprising: (a) at least one complementarity-  
 CC determining region (CDR); or (b) at least heavy chain variable region  
 CC comprising 3 CDRs, and at least one light chain variable region, where  
 CC the CDR has the ability to bind CD33. Also described: (1) an  
 CC immunoconjugate comprising the antibody or its epitope-binding fragment  
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or  
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents a humanised mouse anti-CD33 antibody My9-5 heavy  
 CC chain variable region, which is used in an example from the present  
 CC invention.  
 XX  
 SQ Sequence 118 AA;  
 Query Match 98.6%; Score 613; DB 8; Length 118;  
 Best Local Similarity 98.3%; Pred. No. 1.5e-44;  
 Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGGQGLEWVGVIYFGNDISY 60  
 DB 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGGQGLEWVGVIYFGNDISY 60  
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSEDSAVYTCAREVRLR--YFDVWGAGTTVTSS 118  
 DB 61 NQKPKGKATLTADKSSSTAYMQLSSLTSEDSAVYTCAREVRLR--YFDVWGAGTTVTSS 118  
 RESULT 4  
 ADJ94605  
 ID ADJ94605 standard; protein; 121 AA.  
 XX

AC ADJ94605;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Chimeric anti-CD20 antibody variable heavy chain.  
 XX  
 KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;  
 KW IVIAB variable region; B-cell lymphoma; leukaemia; autoimmune disease;  
 KW thrombocytopenia; lupus; rheumatoid arthritis;  
 KW heavy chain variable region.  
 XX  
 OS Chimeric.  
 OS Unidentified.  
 XX  
 PN WO2003068821-A2.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 14-FEB-2003; 2003WO-GH000665.  
 XX  
 PR 14-FEB-2002; 2002US-0356132P.  
 PR 07-OCT-2002; 2002US-0416232P.  
 XX  
 PA (IMMU-) IMMUNOMEDICS INC.  
 PA (MCCA/) MCCALL J D.  
 XX  
 PI Hansen H, Qu Z, Goldenberg DM;  
 XX WPI; 2003-697522/66.  
 DR N-PSDB; ADJ94604.  
 XX  
 PT New humanized anti-CD20 monoclonal antibody (MAb) that retains  
 PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting  
 PT of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,  
 PT leukemia or an autoimmune diseases.  
 XX  
 PS Disclosure; Fig 2B; 106pp; English.  
 XX  
 CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody  
 CC (MAb) or its antigen-binding fragment containing the complementarity  
 CC determining regions (CDRs) of at least one murine anti-CD20 MAb variable  
 CC region and the framework regions (FRs) of at least one human IVIAB  
 CC variable region. The antibodies of the invention are useful for  
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune  
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The  
 CC present amino acid sequence represents a chimeric anti-CD20 antibody  
 CC variable heavy chain.  
 XX  
 SQ Sequence 121 AA;  
 Query Match 86.3%; Score 536.5; DB 7; Length 121;  
 Best Local Similarity 84.3%; Pred. No. 5e-38;  
 Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;  
 QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGGQGLEWVGVIYFGNDISY 60  
 DB 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGGQGLEWIGAIYFGNGDTSY 60  
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSEDSAVYTCAREVRLR--YFDVWGAGTTVTSS 117  
 DB 61 NQKPKGKATLTADKSSSTAYMQLSSLTSEDSAVYTCAREVRLR--YFDVWGAGTTVTSS 120  
 QY 118 \$ 118  
 DB 121 \$ 121  
 RESULT 5  
 ADJ94607  
 ID ADJ94607 standard; protein; 121 AA.  
 XX  
 ADJ94607;  
 XX

DT 06-MAY-2004 (first entry)  
 XX Chimeric anti-CD20 antibody variable heavy chain amino acid sequence.  
 DE Chimeric anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;  
 KW IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;  
 KW thrombocytopenia; lupus; rheumatoid arthritis;  
 KW heavy chain variable region.  
 XX Chimeric.  
 OS Unidentified.  
 XX WO2003068821-A2.  
 PN 21-AUG-2003.  
 PD 14-FEB-2003; 2003WO-GB000665.  
 PF 14-FEB-2002; 2002US-0356132P.  
 PR 07-OCT-2002; 2002US-0416232P.  
 XX (IMMU-) IMMUNOMEDICS INC.  
 PA (MCCA/) MCCALL J D.  
 XX Hansen H, Qu Z, Goldenberg DM;  
 PI WPI; 2003-697522/66.  
 DR New humanized anti-CD20 monoclonal antibody (MAb) that retains  
 XX substantially the B-cell and B-cell lymphoma and leukemia cell targeting  
 PT of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,  
 PT leukemia or an autoimmune diseases.  
 XX Claim 22; Fig 4A; 106pp; English.  
 PS The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody  
 CC (MAb) or its antigen-binding fragment containing the complementarity  
 CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable  
 CC region and the framework regions (FRs) of at least one human IV1AB  
 CC variable region. The antibodies of the invention are useful for  
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune  
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The  
 CC present amino acid sequence represents a chimeric anti-CD20 antibody  
 CC variable heavy chain.  
 XX Sequence 121 AA;  
 SQ Query Match 86.3%; Score 536.5; DB 7; Length 121;  
 Best Local Similarity 84.3%; Pred. No. 5e-38;  
 Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60  
 DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60  
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSED SAVYICAREVRLR---YFDVWGAGTTVTVS 117  
 DB 61 NQKPKGKATLTADKSSSTAYMQLSSLTSED SAVYICAREVRLR---YFDVWGAGTTVTVS 117  
 QY 118 S 118  
 DB 121 S 121  
 RESULT 6  
 AAR55215  
 ID AAR55215 standard; protein; 140 AA.  
 AC AAR55215;  
 XX 25-MAR-2003 (revised)  
 DT 01-FEB-1995 (first entry)  
 XX

DE Murine variable region heavy chain from 2BS.  
 XX B cell lymphoma chimeric antibody; CD20; peripheral blood cells;  
 KW cell lysis.  
 XX Mus musculus.  
 XX WO9411026-A2.  
 PN 26-MAY-1994.  
 PD 12-NOV-1993; 93WO-US010953.  
 PF 13-NOV-1992; 92US-00978891.  
 PR 03-NOV-1993; 93US-00149099.  
 XX (IDEC-) IDEC PHARM CORP.  
 XX Anderson DR, Rastetter WH, Hanna N, Leonard JE, Newman RA;  
 PI Ref ME;  
 XX WPI; 1994-183162/22.  
 DR N-PSDB; AAQ65631.  
 XX Treating B cell lymphoma with chimeric antibody - against CD20, causing  
 PT rapid depletion of peripheral B cells, also new antibodies and  
 PT hybridomas.  
 XX Disclosure; Fig 5; 101pp; English.  
 PS The sequence is the murine variable region heavy chain derived from  
 CC murine anti-CD20 monoclonal antibody 2BS. See also AAQ65629-35. (Updated  
 CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct  
 CC PI field.)  
 XX Sequence 140 AA;  
 SQ Query Match 85.9%; Score 534.5; DB 2; Length 140;  
 Best Local Similarity 83.5%; Pred. No. 8.6e-38;  
 Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60  
 DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 79  
 QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSED SAVYICAREVRLR---RYFDVWGAGTTVTVS 117  
 DB 80 NQKPKGKATLTADKSSSTAYMQLSSLTSED SAVYICAREVRLR---RYFDVWGAGTTVTVS 139  
 QY 118 S 118  
 DB 140 A 140  
 RESULT 7  
 AAB30694  
 ID AAB30694 standard; protein; 412 AA.  
 XX AAB30694;  
 XX 02-APR-2001 (first entry)  
 DT A fusion of anti-CD20 single chain antibody/streptavidin.  
 XX Streptavidin; tumour cell; cancer; adenocarcinoma;  
 KW hematological malignancy; B9E9.  
 XX Synthetic.  
 OS Streptomyces avidinii.  
 OS Homo sapiens.  
 XX Key  
 FH Protein  
 FT Location/Qualifiers  
 1. .108



FT Peptide /note= "VL chain"  
 FT 109..126  
 FT /note= "linker"  
 FT 127..248  
 FT Protein /note= "VH chain"  
 FT 249..253  
 FT Peptide /note= "linker"  
 FT 254..412  
 FT Protein /note= "streptavidin"  
 FT WO200075333-A1.  
 PN WO200075333-A1.  
 XX 14-DEC-2000.  
 XX 05-JUN-2000; 2000WO-US015595.  
 XX 07-JUN-1999; 99US-0137900P.  
 PR 03-DEC-1999; 99US-0168976P.  
 XX (NEOR-) NEORX CORP.  
 PA Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;  
 PI WPI; 2001-091213/10.  
 XX N-PSDB; AAC86563.  
 DR New vector constructs for expressing genomic streptavidin fusion proteins  
 PT which are useful for targeting tumor cells associated with cancer, e.g.  
 PT adenocarcinomas.  
 XX Example 2; Fig 11B; 100pp; English.  
 PS The present sequence represents a fusion of an anti-CD20 single chain  
 XX antibody (B9E9) streptavidin. The fusion protein is expressed using  
 CC vectors of the invention. The specification describes vector constructs  
 CC for expressing streptavidin fusion proteins. The vector comprises a  
 CC nucleic acid encoding streptavidin or its functional variant operatively  
 CC linked to a promoter, and a cloning site for insertion of a second  
 CC nucleic acid sequence encoding a polypeptide to be fused with  
 CC streptavidin, interposed between the promoter and the first nucleic acid  
 CC sequence. Alternatively, the vector construct comprises a nucleic acid,  
 CC operatively linked to a promoter, encoding a polypeptide to be fused with  
 CC streptavidin, and a cloning site for insertion of a second nucleic acid  
 CC encoding at least 129 amino acids of streptavidin or its functional  
 CC variant. The fusion proteins are useful for targeting tumour cells,  
 CC particularly tumour cells associated with cancer, e.g. adenocarcinomas or  
 CC hematological malignancies. The vector construct is useful for expressing  
 CC of streptavidin fusion proteins. In particular, these are useful as tools  
 CC for medical diagnostics and therapeutic purposes, e.g. for detecting the  
 CC presence or absence of, or treating, a target site within a mammalian  
 CC host  
 XX Sequence 412 AA;  
 SQ Query Match 85.9%; Score 534.5; DB 4; Length 412;  
 Best Local Similarity 85.2%; Pred. No. 2.6e-37;  
 Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;  
 QY 1 QVQLQPGAEVVFPGASVKMSCKASGYTFSTSYIHNIKQTPGQGLEWVGVIYFGNDISY 60  
 Db 128 QVQLVQSGAEVLPFGASVKMSCKASGYTFSTSYNNHWYKQTPGQGLEWIGAIYFGNGDTSY 187  
 QY 61 NQKFKGKATLTADKSSITAYMQLSSLTSEDSAVVYCYAREVRLR----YFDVWGAGTIVTV 116  
 Db 188 NQKFKGKATLTADKSSITAYMQLSSLTSEDSAVVYCYAR-AQLRPNWFYFDVWGAGTIVTV 246  
 QY 117 SS 118  
 Db 247 SS 248

RESULT 8  
 ABJ39009

ID ABJ39009 standard; protein; 412 AA.  
 XX AC ABJ39009;  
 DT 09-OCT-2003 (first entry)  
 XX B9E9 scFvSA fusion protein A amino acid sequence.  
 DE Streptavidin fusion protein; SA; Streptomyces avidinii; biotin; scFvSA;  
 KW anti-CD25 antibody; antigen binding fragment; cytostatic; gene therapy;  
 KW cell-specific targeting agents; single chain; tumour; B9E9.  
 XX Streptomyces avidinii.  
 OS Mus sp.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Region 1..106  
 FT /note= "VL region of the fusion protein"  
 FT Region 107..127  
 FT /note= "Synthetic linker region (PKOD)"  
 FT Region 128..247  
 FT /note= "VH region of the fusion protein"  
 FT Region 248..253  
 FT /note= "Synthetic linker region"  
 FT Region 254..412  
 FT /note= "Streptavidin region of the fusion protein"  
 XX WO2003050260-A2.  
 XX 19-JUN-2003.  
 XX 06-DEC-2002; 2002WO-US039429.  
 XX 07-DEC-2001; 2001US-00013173.  
 PR 17-MAY-2002; 2002US-00150762.  
 PR 16-SEP-2002; 2002US-00244821.  
 XX (NEOR-) NEORX CORP.  
 XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;  
 PI Dearstyne EA;  
 XX WPI; 2003-532908/50.  
 N-PSDB; ABT43498.  
 XX New vector construct for expressing genomic streptavidin fusion proteins  
 PT useful as diagnostic markers or as cell-specific targeting agents.  
 XX Disclosure; Fig 11B; 156pp; English.  
 XX This invention relates to novel vector constructs for the expression of  
 CC streptavidin fusion proteins. Streptavidin (SA) is produced by  
 CC Streptomyces avidinii and specifically binds water-soluble biotin. The  
 CC vectors comprise a nucleic acid sequence encoding genomic streptavidin, a  
 CC promoter operatively linked to the nucleic acid sequence and a cloning  
 CC site for insertion of a second nucleic acid sequence encoding an anti-  
 CC CD25 antibody or its antigen binding fragment. The fusion proteins  
 CC encoded are known as single chain antibody-genomic streptavidin fusion  
 CC proteins (scFvSA). The vectors may have cytostatic activity when used in  
 CC gene therapy. The vectors may be useful in expressing genomic  
 CC streptavidin fusion cassettes. The fusion proteins may be used as  
 CC diagnostic markers or as cell-specific targeting agents. These may also  
 CC be used in treating tumours. The present sequence is the amino acid  
 CC sequence of the B9E9 single chain antibody-genomic streptavidin fusion  
 CC protein of the invention  
 XX Sequence 412 AA;  
 SQ Query Match 85.9%; Score 534.5; DB 6; Length 412;  
 Best Local Similarity 85.2%; Pred. No. 2.6e-37;  
 Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;



CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or  
 CC administering, at a second administration period, a radiolabelled anti-  
 CC CD20 antibody, to the human subject. The invention also discloses  
 CC expression vectors that may be used in the method of the present  
 CC invention. The method is useful for treating B cell lymphoma in humans.  
 CC The present sequence represents murine anti-CD20 antibody heavy chain  
 CC variable region  
 XX  
 SQ Sequence 140 AA;  
 Query Match 85.8%; Score 533.5; DB 6; Length 140;  
 Best Local Similarity 83.5%; Pred. No. 1e-37; Indels 3; Gaps 1;  
 Matches 101; Conservative 8; Mismatches 9;  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDISY 60  
 DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDISY 79  
 QY 61 NQPFKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 117  
 DB 80 NQPFKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 139  
 QY 118 S 118  
 DB 140 A 140  
 RESULT 11  
 ADC66270  
 ID ADC66270 standard; protein; 140 AA.  
 XX  
 AC ADC66270;  
 DT  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Mouse anti-CD20 antibody heavy chain variable region.  
 KW immunosuppressant; cytostatic; antibody; CD20;  
 KW N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine;  
 KW sugar chain; cancer; immune disorder.  
 XX  
 OS Mus musculus.  
 XX  
 PN WC2003055993-A1.  
 XX  
 PD 10-JUL-2003.  
 XX  
 PF 25-DEC-2002; 2002WO-JP019534.  
 XX  
 PR 25-DEC-2001; 2001JP-00392753.  
 PR 09-APR-2002; 2002JP-00106948.  
 PR 01-NOV-2002; 2002JP-00319375.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Shitara K, Sakurada M, Uchida K, Shinkawa T, Satoh M, Nakano R;  
 XX  
 XX WPI; 2003-559274/52.  
 DR N-PSDB; ADC66269.  
 XX  
 PT Antibody binding to CD20 and having Fc-bound sugar chains of low fucose  
 PT content for treatment of cancer and immune disorders.  
 XX  
 PS Disclosure; SEQ ID NO 14; 200pp; Japanese.  
 XX  
 CC The invention relates to cells producing an antibody molecule  
 CC specifically binding to CD20 are new, in which the antibody contains N-  
 CC glycoside bond complex sugar chains bonded to the Fc region of the  
 CC antibody peptide chains, of which less than 20% have a fucose residue  
 CC bonded to the N-acetylglucosamine residue at the reducing end of the  
 CC sugar chain. The cells are used in the treatment and prevention of cancer  
 CC and immune disorders. This sequence corresponds to a protein used in the  
 CC method of the invention.

XX  
 SQ Sequence 140 AA;  
 Query Match 85.8%; Score 533.5; DB 7; Length 140;  
 Best Local Similarity 83.5%; Pred. No. 1e-37; Indels 3; Gaps 1;  
 Matches 101; Conservative 8; Mismatches 9;  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDISY 60  
 DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDISY 79  
 QY 61 NQPFKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 117  
 DB 80 NQPFKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 139  
 QY 118 S 118  
 DB 140 A 140  
 RESULT 12  
 ADE85690  
 ID ADE85690 standard; protein; 140 AA.  
 XX  
 AC ADE85690;  
 DT  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Murine immunoglobulin heavy chain variable region.  
 KW B cell lymphoma; anti-CD20; peripheral B cell; C2B8;  
 KW immunoglobulin heavy chain variable region; mouse; antibody.  
 XX  
 OS Mus sp.  
 XX  
 PN US2003147885-A1.  
 XX  
 PD 07-AUG-2003.  
 XX  
 PF 11-SEP-2002; 2002US-00238681.  
 XX  
 PR 13-NOV-1992; 92US-00978891.  
 PR 03-NOV-1993; 93US-00149099.  
 PR 29-AUG-1997; 97US-00921060.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Anderson DR, Hanna N, Leonard JE, Newman RA, Reiff ME;  
 PI Rastetter WH;  
 XX  
 XX WPI; 2003-897520/82.  
 DR N-PSDB; ADE85689.  
 XX  
 PT Treating B cell lymphoma by administering an anti-CD20 antibody and at  
 PT least one chemotherapeutic agent.  
 XX  
 PS Example; SEQ ID NO 11; 52pp; English.  
 XX  
 CC The invention relates to an improved method for treating B cell lymphoma  
 CC comprising administering an anti-CD20 antibody. The improvement comprises  
 CC administering at least one chemotherapeutic agent. The antibody causes a  
 CC substantial depletion of peripheral B cells. The antibody is chimeric  
 CC anti-CD20 or C2B8. The method is useful for treating B cell lymphoma.  
 CC This sequence represents a murine immunoglobulin heavy chain variable  
 CC region used in the method of the invention.  
 XX  
 SQ Sequence 140 AA;  
 Query Match 85.8%; Score 533.5; DB 7; Length 140;  
 Best Local Similarity 83.5%; Pred. No. 1e-37; Indels 3; Gaps 1;  
 Matches 101; Conservative 8; Mismatches 9;  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDISY 60

```

Db      20 QVQLQPGAEIVKPGASVKMSCKASGYTFTSYNMHWVKQTTPGRGLEWIGAIYPGNGDTSY 79
      61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTS 117
      80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTS 139

QY      118 S 118
      140 A 140

Db      118 S 118
      140 A 140

RESULT 13
ADE73084
ID ADE73084 standard; protein; 140 AA.
XX
AC ADE73084;
XX
DT 29-JAN-2004 (first entry)
XX
DE Murine FUT8-related sequence.
XX
KW Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial;
KW Antiviral; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour;
KW allergy; inflammation; autoimmune disease; circulatory disorder;
KW viral infection; bacterial infection; murine.
XX
OS Mus musculus.
XX
PN WO2003085107-A1.
XX
PD 16-OCT-2003.
XX
PF 09-APR-2003; 2003WO-JP004507.
XX
PR 09-APR-2002; 2002JP-00106953.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Yamane N, Satoh M, Mori K, Yamano K;
XX
WPI: 2003-833570/77.
DR N-PSDB; ADE73069.
XX
PT Cells with reduced or absent alpha 1,6-fucosyltransferase activity for
PT treatment of tumors, allergy, inflammation, autoimmune disease,
PT circulatory disorders, and viral and bacterial infection.
XX
PS Example 6; Page 165-166; 187pp; Japanese.
XX
CC The present invention relates to cells with modified sugar chain
CC modifying enzyme activity. The enzyme activity of binding the 1-position
CC of fucose to the 6-position of an N-acetylglucosamine at the reducing end
CC of a complex N-glycoside linked sugar chain via an alpha-bond is absent
CC or less than in the parent cell. The sugar chain modifying enzyme is
CC preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-
CC ADE73056). The invention is useful for the treatment and prevention of
CC tumours, allergy, inflammation, autoimmune disease, circulatory
CC disorders, and viral and bacterial infection. The present sequence was
CC used in an example from the invention.
XX
SQ Sequence 140 AA;
Query Match 85.8%; Score 533.5; DB 7; Length 140;
Best Local Similarity 83.5%; Pred. No. 1e-37;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY      1 QVQLQPGAEIVKPGASVKMSCKASGYTFTSYIHWIKQTTPGGLWVGVIYPGNDISY 60
      20 QVQLQPGAEIVKPGASVKMSCKASGYTFTSYNMHWVKQTTPGRGLEWIGAIYPGNGDTSY 79
      61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTS 117
      80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTS 139

```

```

Db      80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTS 139
      118 S 118
      140 A 140

QY      118 S 118
      140 A 140

Db      118 S 118
      140 A 140

RESULT 14
ADF60661
ID ADF60661 standard; protein; 140 AA.
XX
AC ADF60661;
XX
DT 12-FEB-2004 (first entry)
XX
DE Protein related to the invention #2.
XX
KW Cytostatic; antiallergic; immunomodulator; cardiant; virucide;
KW antibacterial; drug; antibody; lectin; N-acetylglucosamine; fucose;
KW tumour; allergy; inflammation; autoimmune disease; circulatory system;
KW viral; bacterial; infection; CCR4.
XX
OS Mus musculus.
XX
PN WO2003084569-A1.
XX
PD 16-OCT-2003.
XX
PF 09-APR-2003; 2003WO-JP004503.
XX
PR 09-APR-2002; 2002JP-00106949.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Niwa R, Shitara K;
XX
WPI: 2003-812676/76.
DR N-PSDB; ADF60652.
XX
PT Drugs containing antibody compositions produced by cells tolerant to
PT lectin recognizing specific sugar-chain structure, useful in screening
PT and treating patients not suitable for drugs not derived from these
PT cells.
XX
PS Disclosure; SEQ ID NO 13; 157pp; Japanese.
XX
CC The invention relates to a drug containing as the active ingredient, an
CC antibody composition produced by cells tolerant to a lectin recognising a
CC sugar-chain structure in which an alpha-bond is formed between the 6-
CC position of N-acetylglucosamine at the reducing end of an N-glycoside
CC bond-type complex sugar chain and the 1-position of fucose. The drugs are
CC useful in screening and treating patients not suitable for drugs not
CC derived from these cells. They are particularly useful as diagnostics,
CC preventives or remedies for diseases accompanying tumour, allergy or
CC inflammation, autoimmune diseases, diseases of the circulatory system,
CC and viral or bacterial infections. In a method from the invention, a CCR4
CC gene was used for constructing a vector (CAG-CCR4/pcDNA3) for producing a
CC transfectant EL-4 cell (ATCC TIB-39) to express chimeric CCR4. Antibody-
CC dependent cytotoxicity of the thus produced antibody composition was
CC confirmed. The current sequence represents a protein related to the
CC invention.
XX
SQ Sequence 140 AA;
Query Match 85.8%; Score 533.5; DB 7; Length 140;
Best Local Similarity 83.5%; Pred. No. 1e-37;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY      1 QVQLQPGAEIVKPGASVKMSCKASGYTFTSYIHWIKQTTPGGLWVGVIYPGNDISY 60
      20 QVQLQPGAEIVKPGASVKMSCKASGYTFTSYNMHWVKQTTPGRGLEWIGAIYPGNGDTSY 79
      61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTS 117
      80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTS 139

```

Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICARSTYYGDDWYFNWVGACTTIVTS 139  
Qy 118 S 118  
Db 140 A 140

RESULT 15

ADN49734

ID ADN49734 standard; protein; 140 AA.

AC ADN49734;

XX

XX

15-JUL-2004 (first entry)

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Qy 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICAREVRLR---YFDVWGACTTIVTS 117  
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICARSTYYGDDWYFNWVGACTTIVTS 139  
Qy 118 S 118  
Db 140 A 140

Search completed: May 9, 2006, 01:25:28  
Job time : 107.251 secs

Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICARSTYYGDDWYFNWVGACTTIVTS 139  
Qy 118 S 118  
Db 140 A 140

RESULT 15

ADN49734

ID ADN49734 standard; protein; 140 AA.

AC ADN49734;

XX

XX

15-JUL-2004 (first entry)

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICARSTYYGDDWYFNWVGACTTIVTS 139  
Qy 118 S 118  
Db 140 A 140

RESULT 15

ADN49734

ID ADN49734 standard; protein; 140 AA.

AC ADN49734;

XX

XX

15-JUL-2004 (first entry)

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICARSTYYGDDWYFNWVGACTTIVTS 139  
Qy 118 S 118  
Db 140 A 140

RESULT 15

ADN49734

ID ADN49734 standard; protein; 140 AA.

AC ADN49734;

XX

XX

15-JUL-2004 (first entry)

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICARSTYYGDDWYFNWVGACTTIVTS 139  
Qy 118 S 118  
Db 140 A 140

RESULT 15

ADN49734

ID ADN49734 standard; protein; 140 AA.

AC ADN49734;

XX

XX

15-JUL-2004 (first entry)

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:25:51 ; Search time 17.8788 Seconds  
(without alignments)  
635.031 Million cell updates/sec

Title: US-10-700-632-7  
Perfect score: 622  
Sequence: 1 QVQLQQPGAEVVKPGASVKM.....EVRLRYFDVWVGAGTTVTSS 118  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	494	79.4	120	2 B22769	Ig heavy chain V r
2	491.5	79.0	119	2 PL0089	Ig heavy chain V r
3	484	77.8	118	2 S38717	Ig heavy chain V r
4	483	77.7	120	2 G28195	Ig heavy chain V r
5	481.5	77.4	138	2 E32513	Ig heavy chain pre
6	480.5	77.3	120	2 S25175	Ig heavy chain V r
7	480.5	77.3	136	2 PL0208	Ig heavy chain pre
8	479.5	77.1	117	1 MHMS75	Ig heavy chain V r
9	477.5	76.8	138	2 S21810	Ig heavy chain V r
10	476	76.5	101	2 S42184	Ig gamma chain V r
11	476	76.5	101	2 S42179	Ig gamma chain V r
12	476	76.5	102	2 S42180	Ig gamma chain V r
13	475	76.4	115	2 A54378	Ig heavy chain V r
14	473.5	76.1	117	1 MHMS4E	Ig heavy chain V r
15	473.5	76.1	140	2 T01407	Ig heavy chain (my
16	473	76.0	120	2 F28195	Ig heavy chain V r
17	471	75.7	115	2 C27563	Ig heavy chain V r
18	469	75.4	131	2 S66537	Ig heavy chain V r
19	468.5	75.3	123	2 S20646	Ig heavy chain V r
20	468	75.2	139	1 MHMS18	Ig heavy chain pre
21	468	75.2	287	4 PC1402	peIB leader/Ig hea
22	466	74.9	116	2 S53751	antibody Fab Jel 1
23	466	74.9	135	2 A30577	Ig heavy chain pre
24	465	74.8	133	2 PC1155	Ig heavy chain pre
25	464.5	74.7	246	2 S38950	Ig gamma chain - m
26	464.5	74.7	446	2 S40295	Ig gamma-2a chain
27	464	74.6	120	2 S41394	Ig heavy chain V r
28	464	74.6	141	2 A39276	Ig heavy chain pre
29	462	74.3	137	1 G2MS43	Ig heavy chain pre

ALIGNMENTS

RESULT 1

B22769  
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)

C;Species: Mus musculus (house mouse)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 16-Aug-1996  
C;Accession: B22769  
R;Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.  
EMBO J. 1, 635-640, 1982  
A;Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between A;Reference number: A90971; MUID:84236026; PMID:7188353  
A;Accession: B22769  
A;Molecule type: protein  
A;Residues: 1-120 <DIL>

A;Cross-references: UNIPARC:UPI0000176B76

A;Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V  
A;Note: peptides and unsequenced residues were positioned by homology with the B1-8 seq  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 494; DB 2; Length 120;  
Best Local Similarity 77.5%; Pred. No. 4.7e-37;  
Matches 93; Conservative 11; Mismatches 14; Indels 2; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGVTFTSYTHIKOTPGQGLEWVGVIYPCNDISY 60  
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGVTFTSYTHIKOTPGQGLEWVGVIYPCNDISY 60  
Qy 61 NQKFKGKATLTADKSTTAYMQLSLTSDSAYVYCAR--EVRLRYFDVWVGAGTTVTSS 118  
Db 61 NQKFKGKATLTADKSTTAYMQLSLTSDSAYVYCARVYDYGGSSYFDYWGQGTTLTVSS 120

RESULT 2

PL0089

Ig heavy chain V region (12S18-1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Mar-2000  
C;Accession: PL0089  
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.;  
J. Exp. Med. 169, 519-533, 1989

A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s ar  
A;Reference number: PL0080; MUID:89094248; PMID:2492056  
A;Accession: PL0089

A;Molecule type: mRNA

A;Residues: 1-119 <ME>

A;Cross-references: UNIPARC:UPI0000115F1B; GB:X58580; GB:Y00794; NID:G51591; PIDN:CAA41

A;Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal an  
A;Note: sequences from two other clones (18S28-16 and 12884-3) were almost identical to  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>



```
Query Match      79.0%; Score 491.5; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 7.8e-37;
Matches 93; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGNDISY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGSDYNY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKGKATLTADKSSSTAYMQLSSTSDSAVYFCAREGSEYDEADYWGKGTTLTVSS 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NEKFKSKATLTVDTSSTAYMQLSSTSDSAVYFCAREGSEYDEADYWGKGTTLTVSS 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
S38717
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38717
R:Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38717
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <C1M>
A:Cross-references: UNIPARC:UPI0000117541; EMBL:X76020; NID:g416099; PIDN:CAAS3607.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      77.8%; Score 484; DB 2; Length 118;
Best Local Similarity 77.1%; Pred. No. 3.6e-36;
Matches 91; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGNDISY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QDQLQSGPDLVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGNDISY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKGKATLTADKSSSTAYMQLSSTSDSAVYFCAREVRLRYFDVMGAGTTLTVSS 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKGKATLTADKSSSTAYMQLSSTSDSAVYFCARENGNFYFDYWGQGTTLTVSS 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
G28195
Ig heavy chain V region (anti-haloperidol antibody B) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C:Accession: G28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid e
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: G28195
A:Molecule type: mRNA
A:Residues: 1-120 <SHE>
A:Cross-references: UNIPARC:UPI0000114D6F; GB:M19772; NID:g195520; PIDN:AAA38340.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      77.7%; Score 483; DB 2; Length 120;
Best Local Similarity 76.7%; Pred. No. 4.5e-36;
Matches 92; Conservative 10; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGNDISY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQSGPDLVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGNDISY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKGKATLTADKSSSTAYMQLSSTSDSAVYFCAREVRLRYFDVMGAGTTLTVSS 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Query Match      77.4%; Score 481.5; DB 2; Length 138;
Best Local Similarity 75.8%; Pred. No. 7e-36;
Matches 91; Conservative 14; Mismatches 12; Indels 3; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGNDISY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGSSNTY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKGKATLTADKSSSTAYMQLSSTSDSAVYFCAREVRLRYFDVMGAGTTLTVSS 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKFKSKATLTVDTSSTAYMQLSSTSDSAVYFCARELRYRYAMDYWGQGTTLTVSS 138
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S25175
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25175
R:Monestier, M.; Fasy, T.M.; Lozman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histone
A:Reference number: S25174
A:Accession: S25175
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MON>
A:Cross-references: UNIPARC:UPI00001160C2; EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      77.3%; Score 480.5; DB 2; Length 120;
Best Local Similarity 75.8%; Pred. No. 7.5e-36;
Matches 91; Conservative 10; Mismatches 16; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGNDISY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGGLWGVVYPGSDSETHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKGKATLTADKSSSTAYMQLSSTSDSAVYFCAREVRLRYFDVMGAGTTLTVSS 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKGKATLTVDKSSNTAYMQLSSTSDSAVYFCAREKTDYNYFDYWGQGTTLTVS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
PL0208
Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/c)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C:Accession: PL0208
R:Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
```

Eusebio, J. Immunol. 23, 2503-2510, 1993.  
 A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spe-  
 A:Reference number: S42176; MUID:94009207; PMID:7691608  
 A:Accession: S42179  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-101 <NOJ>  
 A:Cross-references: UNIPARC:UPI000011655F; EMBL:Z25447; NID:g407816; PIDN:CAAB0934.1; P  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 476; DB 2; Length 101;  
Best Local Similarity 90.7%; Pred. No. 1.6e-35;  
Matches 88; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61  
DB 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61

QY 62 QKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAR 98  
DB 62 QKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAR 98

RESULT 12  
S42180  
Ig gamma chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change 23-Jul-1999  
C;Accession: S42180  
R;No, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993  
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with speed  
A;Reference number: S42176; MUID:9409207; PMID:7691608  
A;Accession: S42180  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-102 <MOJ>  
A;Cross-references: UNIPARC:UPI0000116561; EMBL:225449; NID:G407818; PIDN:CAA80936.1; PIDN:CAA80936.1; PIDN:CAA80936.1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 476; DB 2; Length 102;  
Best Local Similarity 90.7%; Pred. No. 1.6e-35;  
Matches 88; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61  
DB 2 VOLQOPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISYN 61

QY 62 QKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAR 98  
DB 62 QKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAR 98

RESULT 13  
A54378  
Ig heavy chain V region anti-triplex DNA - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C;Accession: A54378  
R;Agarie, Y.M.; Lee, J.S.; Burkholder, G.D.  
J. Biol. Chem. 269, 7019-7023, 1994  
A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence  
A;Reference number: A54378; MUID:94165109; PMID:7509814  
A;Accession: A54378  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-115 <AGA>  
A;Cross-references: UNIPARC:UPI0000176E3F; GB:S68981; NID:G545744; PIDN:AAB30095.1; PIDN:AAB30095.1; PIDN:AAB30095.1  
A;Experimental source: spleen and myeloma cell line MOPC 315.43  
A;Note: sequence inconsistent with nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBI:144172, NCBIP:144173)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 475; DB 2; Length 115;  
Best Local Similarity 75.7%; Pred. No. 2.2e-35;  
Matches 87; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60  
DB 1 EVLQQSGPELVKPGASVIRISCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNGNTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVMGAGTTVT 115  
DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSSGGYLYGWGQGTTLT 115

RESULT 14  
MMS4E  
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Nov-1979 #sequence\_revision 14-Nov-1993 #text\_change 09-Jul-2004  
C;Accession: A02039  
R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.  
Biochemistry 21, 5415-5424, 1982  
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain c  
A;Reference number: A02039; MUID:83075344; PMID:6816276  
A;Accession: A02039  
A;Molecule type: protein  
A;Residues: 1-117 <KEH>  
A;Cross-references: UNIPROT:P01756; UNIPARC:UPI00000270F1  
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context  
C;Comment: This protein binds dextran.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: glycoprotein; heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;22-96/Diulfide bonds: #status predicted  
F;55/Binding site: carbohydrate (Asn) (covalent) #status atypical

Query Match 76.1%; Score 473.5; DB 1; Length 117;  
Best Local Similarity 77.1%; Pred. No. 3e-35;  
Matches 91; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60  
DB 1 EVLQQSGPELVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNGNTSY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVMGAGTTVTSS 118  
DB 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCARDYDW-YFDVMGAGTTVTSS 117

RESULT 15  
T01407  
Ig heavy chain (myeloma M104E) - mouse (fragment)  
C;Species: Mus sp. (mouse)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C;Accession: T01407  
R;Takahashi, S.; Matsura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamanot  
Microbiol. Immunol. 36, 855-863, 1992  
A;Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and  
A;Reference number: Z14317; MUID:93116638; PMID:1474935  
A;Accession: T01407  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-140 <TAK>  
A;Cross-references: UNIPARC:UPI000011B29E; EMBL:S51851; NID:G262657  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 76.1%; Score 473.5; DB 2; Length 140;  
Best Local Similarity 77.1%; Pred. No. 3.6e-35;  
Matches 91; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60  
DB 20 EVLQQSGPELVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNGNTSY 79

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVMGAGTTVTSS 118  
DB 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCARDYDW-YFDVMGAGTTVTSS 136

Search completed: May 9, 2006, 01:33:51  
Job time : 18.8788 secs

**THIS PAGE BLANK (uspto)**



```
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN Name=VH186.2-D-J-C mu; Synonym=V304-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX -taxid=911
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -; mRNA.
DR EMBL; AB069914; BAB63930.1; -; mRNA.
DR PIR; S26744; S26744.
DR HSP; P01751; IAGW.
DR SMR; Q91V67; 1-129.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBP CRC64;

Query Match 79.6%; Score 495; DB 2; Length 143;
Best Local Similarity 78.8%; Pred. No. 9.6e-45;
Matches 93; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQQPAGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTQPGQGLEWVGVIYPGNDDISY 60
Db 1 QVQLQQPAGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTQPGQGLEWVGVIYPGNDDISY 60
QY 61 NQKPKGKATLTADKSSSTAYMQLSSLTSEDNAVYICAREVRLRYFDVVGAGTTVTVSS 118
Db 61 NQKPKGKATLTADKSSSTAYMQLSSLTSEDNAVYICAREVRLRYFDVVGAGTTVTVSS 118

RESULT 3
Q924Q0_MOUSE
ID Q924Q0_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924Q0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784 (1988).
DR EMBL; AB067795; BAB63280.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSP; P01751; IAGW.
DR SMR; Q924Q0; 1-134.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;
```



```
Query Match 78.6%; Score 489; DB 2; Length 143;
Best Local Similarity 77.1%; Pred. No. 4.2e-44;
Matches 91; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHLIKOTPGQGLEWVGVIYPCNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHLIKOTPGQGLEWVGVIYPCNDISY 60
QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTITVTSS 118
DB 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTITVTSS 118

RESULT 5
Q8VCX7 MOUSE
ID Q8VCX7 MOUSE PRELIMINARY; PRT; 613 AA.
AC Q8VCX7
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Names=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2464031;
RA Sikder S.K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
RA Morrison S.L., Kabat E.A.;
RT "Amino acid substitutions in VH CDR2 change the idiotype but not the
antigen-binding of monoclonal antibodies to alpha(1----6)dextran.";
RL J. Immunol. 142:888-893(1989).
DR EMBL; BC018315; AAH18315.1; -; mRNA.
DR PIR; C30562; C30562.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
```

```
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0000187; P:activation of MAPK activity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. .; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 77.8%; Score 484; DB 2; Length 613;
Best Local Similarity 76.3%; Pred. No. 8e-43;
Matches 90; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHLIKOTPGQGLEWVGVIYPCNDISY 60
DB 20 QVQLQSGAEIMKPGASVKISCKATGYTSSWIEWKQPGHLEWIEILPGSGSTNY 79
QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTITVTSS 118
DB 80 NEKFKGKATFTADTSSNTAYMQLSSLTSDSAVYVCARRLGRWYFDVWGAGTITVTSS 137

RESULT 6
HV13 MOUSE
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
bind dextran differ from that shown at 1-7 positions, many of
which occur in the D and J segments.
CC -!- MISCELLANEOUS: This protein binds dextran.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC PIR; A26242; MHMSJ5.
DR HSSP; P01751; 1NOB.
DR SMR; P01757; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
```

✓



```
DR PIR; PH1153; PH1153.
DR HSP; P01751; 1A6W.
DR SMR; Q924R8; 1-137.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460F1DF1B7538 CRC64;

Query Match 76.4%; Score 475.5; DB 2; Length 146;
Best Local Similarity 74.4%; Pred. No. 1.2e-42;
Matches 90; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKTPQGLEWVGVIYPGNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKTPQGLEWVGVIYPGNDISY 60
QY 61 NQKFKGKATLTADKSTTAYMQLSLTSDSAVYYCAREV---RLRYFDVWGAGTTVTVS 117
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYYCARSYVYDYGQGTTLTVS 120
QY 118 $ 118
DB 121 $ 121

RESULT 11
Q91VA2 MOUSE
ID Q91VA2 MOUSE PRELIMINARY; PRT; 143 AA.
AC Q91VA2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067786; BAB63271.1; -; mRNA.
DR EMBL; AB069911; BAB63927.1; -; mRNA.
DR PIR; PH1105; PH1105.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR HSP; P01751; 1A6W.
DR SMR; Q91VA2; 1-134.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143

SQ SEQUENCE 143 AA; 15617 MW; 51952152F6F3AD47 CRC64;

Query Match 76.2%; Score 474; DB 2; Length 143;
Best Local Similarity 74.6%; Pred. No. 1.7e-42;
Matches 88; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKTPQGLEWVGVIYPGNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKTPQGLEWVGVIYPGNDISY 60
QY 61 NQKFKGKATLTADKSTTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTVS 118
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYYCARSYVGAFDVWGTTVTVS 118

RESULT 12
HV12 MOUSE
ID HV12 MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC 1- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma
CC protein has also been determined.
CC 2- MISCELLANEOUS: This protein binds dextran.
CC 3- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; A02039; MHMS4E.
DR HSP; P01751; 1NOB.
DR SMR; P01756; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT CARBOHYD 55 55 N-linked (GlcNAc...) (complex).
FT DISULFID 22 96 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 76.1%; Score 473.5; DB 1; Length 117;
Best Local Similarity 77.1%; Pred. No. 1.5e-42;
Matches 91; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKTPQGLEWVGVIYPGNDISY 60
DB 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTSYIHWIKTPQGLEWVGVIYPGNDISY 60
QY 61 NQKFKGKATLTADKSTTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTVS 118
DB 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYYCARDYD-W-YFDVWGAGTTVTVS 117
```

```
RESULT 13
Q5BJZ2_RAT PRELIMINARY; PRT; 458 AA.
AC Q5BJZ2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091272; AAH91272.1; -; mRNA.
DR SRR; Q5BJZ2; 21-454.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match 76.08; Score 472.5; DB 2; Length 458;
Best Local Similarity 76.08; Pred. No. 9.6e-42;
Matches 92; Conservative 9; Mismatches 13; Indels 7; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKSCASGVTFSTSYTHWIKOTPGGLEWVGVIYPCNDISY 60
DB 20 QVQLQSGAEVLPFGSSVKISCRASGYTFNTHWIKQPGNGLEWIGWIFPGNGTKY 79

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICAREVRLRYFDVWGAGTTVTVS 117
DB 80 NQKFNKGKATLTADKSSSTAYMQLSSLTSEDSAVYICAREVRLRYFDVWGAGTTVTVS 135
```

```
QY 118 S 118
DB 136 S 136

RESULT 14
Q921C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q921C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mab 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells.";
RL Mol. Immunol. 34:441-452 (1997).
DR EMBL; U79801; AAD00293.1; -; mRNA.
DR HSSP; P01751; INQB.
DR SRR; Q921C4; 1-118.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
DR NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13036 MW; 90E5C559D31EC4FC CRC64;

Query Match 75.98; Score 472; DB 2; Length 118;
Best Local Similarity 73.78; Pred. No. 2.2e-42;
Matches 87; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKSCASGVTFSTSYTHWIKOTPGGLEWVGVIYPCNDISY 60
DB 1 QVQLQSGAEVLPFGSSVKISCRASGYTFNTHWIKQPGNGLEWIGWIFPGNGTKY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYICAREVRLRYFDVWGAGTTVTVS 118
DB 61 TQKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYICAREVRLRYFDVWGAGTTVTVS 118

RESULT 15
Q924P5_MOUSE PRELIMINARY; PRT; 144 AA.
AC Q924P5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
```

DR EMBL; AB069920; BAB63936.1; -; mRNA.  
DR PIR; PH1137; PH1137.  
DR PIR; S26744; S26744.  
DR HSSP; P01751; 1A6W.  
DR SMR; Q924P5; 1-135.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 15865 MW; CD07BE97E95C1B27 CRC64;

Query Match 75.6%; Score 470.5; DB 2; Length 144;  
Best Local Similarity 75.6%; Pred. No. 4e-42;  
Matches 90; Conservative 10; Mismatches 18; Indels 1; Gaps 1;  
  
QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYPGNDDISY 60  
DB 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYPGNDDISY 60  
  
QY 61 NQKFKGKATLTADKSTTAYMQLSSLTSDSAVYYCAR-EVRLRYFDVWGAGTTVTVSS 118  
DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYYCASVYSSVYFDVWGTGTTVTVSS 119

Search completed: May 9, 2006, 01:32:36  
Job time : 109.039 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:32:56 ; Search time 26.5628 Seconds  
(without alignments)  
367.271 Million cell updates/sec

Title: US-10-700-632-7  
Perfect score: 622  
Sequence: 1 QVQLQPGAEVVRKPGASVKM.....EVLRLYFDVWGAGTTVTVSS 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.5	85.8	140	2	US-08-475-815B-11
2	533.5	85.8	470	2	Sequence 11, Appl
3	525.5	84.5	140	1	US-09-238-741-4
4	525.5	84.5	140	1	Sequence 4, Appl
5	510.5	82.1	121	2	US-08-476-275-6
6	510.5	82.1	121	2	Sequence 6, Appl
7	510.5	82.1	121	2	US-08-475-813-6
8	503	80.9	140	4	Sequence 7, Appl
9	503	80.9	140	4	Sequence 4, Appl
10	502.5	80.8	140	2	Sequence 44, Appl
11	501	80.5	257	2	Sequence 44, Appl
12	500	80.4	118	2	Sequence 4, Appl
13	493	79.3	273	1	Sequence 113, App
14	488.5	78.5	135	1	Sequence 48, Appl
15	488.5	78.5	274	1	Sequence 18, Appl
16	478.5	77.1	119	1	Sequence 4, Appl
17	478.5	76.9	119	1	Sequence 12, Appl
18	477.5	76.8	117	2	Sequence 121, App
19	476.5	76.6	288	2	Sequence 2, Appl
20	476.5	76.6	673	2	Sequence 38, Appl
21	475.5	76.4	119	2	Sequence 32, Appl
22	472.5	76.0	119	2	Sequence 60, Appl
23	472.5	76.0	445	1	Sequence 10, Appl
24	472.5	76.0	464	1	Sequence 33, Appl
25	471.5	75.8	119	2	Sequence 36, Appl
26	471	75.7	117	2	Sequence 62, Appl
27	471	75.7	117	2	Sequence 15, Appl
					Sequence 15, Appl

Sequence 72, Appl  
Sequence 3, Appl  
Sequence 9, Appl  
Sequence 7, Appl  
Sequence 5, Appl  
Sequence 63, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 7, Appl  
Sequence 9, Appl  
Sequence 24, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 27, Appl  
Sequence 61, Appl

28 471 75.7 269 1 US-08-428-257A-72  
29 471 75.7 269 1 US-08-491-988-3  
30 471 75.7 402 1 US-08-491-988-9  
31 471 75.7 415 1 US-08-491-988-7  
32 471 75.7 435 1 US-08-491-988-5  
33 470.5 75.6 119 2 US-08-881-037-63  
34 470 75.6 122 1 US-08-236-520-9  
35 470 75.6 122 4 PCT-US95-05262-9  
36 469.5 75.5 143 1 US-08-236-520-7  
37 469.5 75.5 143 4 PCT-US95-05262-7  
38 468.5 75.3 140 1 US-07-946-421-24  
39 468 75.2 114 2 US-09-344-587-10  
40 468 75.2 122 2 US-10-092-246-10  
41 468 75.2 122 2 US-10-092-246-11  
42 468 75.2 122 2 US-10-096-246A-10  
43 468 75.2 122 2 US-10-096-246A-11  
44 467.5 75.2 117 2 US-08-913-555-27  
45 467.5 75.2 119 2 US-08-881-037-61

## ALIGNMENTS

## RESULT 1

US-08-475-815B-11  
; Sequence 11, Application US/08475815B  
; Patent No. 6399061  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL R.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: LEONARD, JOHN E.  
; APPLICANT: NEWMAN, ROLAND A.  
; APPLICANT: REFF, MITCHELL E.  
; APPLICANT: RASTETTER, WILLIAM H.  
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND  
; TITLE OF INVENTION: RADIO-LABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY WINTHROP  
; STREET: 1100 New York Avenue, N.W., Ninth FL.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,815B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,099  
; FILING DATE: 03-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 23522-0157  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 140 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear



```

; MOLECULE TYPE: protein
US-08-475-815B-11

Query Match      85.8%; Score 533.5; DB 2; Length 140;
Best Local Similarity 83.5%; Pred. No. 1.8e-42;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPOGGLWGVVYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPOGGLWGVVYPGNDISY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
   :
Db 140 A 140

RESULT 2
US-09-238-741-4
; Sequence 4, Application US/09238741
; Patent No. 6897044
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKY, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABARRE, MICHAEL J.
; APPLICANT: LUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/09/238,741
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match      85.8%; Score 533.5; DB 2; Length 470;
Best Local Similarity 83.5%; Pred. No. 6.5e-42;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPOGGLWGVVYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPOGGLWGVVYPGNDISY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
   :
Db 140 A 140

RESULT 3
US-08-476-275-6
; Sequence 6, Application US/08476275
; Patent No. 5776456
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
```

```

; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
; TITLE OF INVENTION: Lymphoma
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,275
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-275-6

Query Match      84.5%; Score 525.5; DB 1; Length 140;
Best Local Similarity 82.6%; Pred. No. 9.8e-42;
Matches 100; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPOGGLWGVVYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPOGGLWGVVYPGNDISY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
   :
Db 140 A 140

RESULT 4
US-08-475-813-6
; Sequence 6, Application US/08475813
; Patent No. 6682734
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Leonard, John E.
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: Therapeutic Application of Chimeric and
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
```





SOFTWARE: PatentIn Release #1.0, Version #1.25

SEQ ID NO 113  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic, no  
OTHER INFORMATION: natural origin  
US-09-419-788-113

Query Match 80.5%; Score 501; DB 2; Length 257;  
Best Local Similarity 80.5%; Pred. No. 3.6e-39;  
Matches 95; Conservative 9; Mismatches 8; Indels 6; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPOGLEWGVVYFGNDISY 60  
Db 3 EVQLQSGAELVKPGASVKMSCKASGYTFTSYIHWIKQTPOGLEWGVVYFGNDISY 62

QY 61 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTV 118  
Db 63 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTV 114

RESULT 12  
US-08-766-350B-48  
Sequence 48, Application US/08766350B  
Patent No. 6949244  
GENERAL INFORMATION:  
APPLICANT: Chatterjee, Malaya  
Foon, Kenneth A.  
Chatterjee, Sunil K.  
TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,350B  
FILING DATE: 13-Dec-1996  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Polizzi, Catherine M.  
REGISTRATION NUMBER: 40,130  
REFERENCE/DOCKET NUMBER: 30414-20003.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
US-08-766-350B-48

Query Match 80.4%; Score 500; DB 2; Length 118;  
Best Local Similarity 78.8%; Pred. No. 1.9e-39;  
Matches 93; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPOGLEWGVVYFGNDISY 60  
Db 1 QVQLQSGAELVKPGASVKMSCKASGYTFTSYIHWIKQTPOGLEWGVVYFGNDISY 60

QY 61 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTV 118  
Db 61 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTV 118

RESULT 13  
US-08-403-853-18  
Sequence 18, Application US/08403853  
Patent No. 5844094  
GENERAL INFORMATION:  
APPLICANT: HUDSON, Peter J.  
APPLICANT: LAH, Maria  
APPLICANT: KORRT, Alex A.  
APPLICANT: IRVING, Robert A.  
APPLICANT: ATWELL, John L.  
APPLICANT: MALBY, Robyn L.  
APPLICANT: POWER, Barbara E.  
APPLICANT: COLMAN, Peter M.  
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,853  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL 4973  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-403-853-18

Query Match 79.3%; Score 493; DB 1; Length 273;  
Best Local Similarity 78.5%; Pred. No. 2.2e-38;  
Matches 95; Conservative 9; Mismatches 13; Indels 4; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPOGLEWGVVYFGNDISY 60  
Db 23 QVQLQSGAELVKPGASVKMSCKASGYTFTSYIHWIKQTPOGLEWGVVYFGNDISY 82

QY 61 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTV 116  
Db 83 NQKPKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLRYFDVWGAGTTVTV 142

QY 117 S 117



**THIS PAGE BLANK (uspto)**



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:57:07 ; Search time 88.6277 Seconds  
(without alignments)

556.303 Million cell updates/sec

Title: US-10-700-632-7

Perfect score: 622

Sequence: 1 QVQLQPGAEVVKPGASVKM.....EVRLRYFDVWGAGTTVTYSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_Main.\*  
1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622	100.0	118	5	US-10-700-632-7
2	618	99.4	117	5	US-10-700-632-73
3	613	98.6	118	5	US-10-700-632-9
4	536.5	86.3	121	4	US-10-366-709-39
5	534.5	85.9	412	4	US-10-013-173-6
6	534.5	85.9	412	4	US-10-150-762-6
7	534.5	85.9	412	4	US-10-244-821-6
8	533.5	85.8	140	4	US-10-238-681-11
9	533.5	85.8	140	4	US-10-411-037-62
10	533.5	85.8	140	4	US-10-411-026-62
11	533.5	85.8	140	4	US-10-410-962-62
12	533.5	85.8	140	4	US-10-411-049-62
13	533.5	85.8	140	4	US-10-327-663-14
14	533.5	85.8	140	4	US-10-410-930-62
15	533.5	85.8	140	4	US-10-410-997-62
16	533.5	85.8	140	4	US-10-411-012-62
17	533.5	85.8	140	4	US-10-287-994-62
18	533.5	85.8	140	4	US-10-410-913-62
19	533.5	85.8	140	5	US-10-723-003-36
20	533.5	85.8	140	5	US-10-410-980-62
21	533.5	85.8	140	5	US-10-410-897-62
22	533.5	85.8	140	5	US-10-492-261-62
23	533.5	85.8	140	6	US-11-004-639-36
24	533.5	85.8	368	5	US-10-880-028-47
25	533.5	85.8	368	5	US-10-880-320-47
26	533.5	85.8	451	5	US-10-822-231-4
27	533.5	85.8	451	5	US-10-822-231-5

```

28 533.5 85.8 470 5 US-10-723-003-40 Sequence 40, Appl
29 533.5 85.8 470 6 US-11-019-180-4 Sequence 4, Appl
30 533.5 85.8 470 6 US-11-004-639-40 Sequence 40, Appl
31 533.5 85.8 626 5 US-10-723-003-44 Sequence 44, Appl
32 533.5 85.8 626 6 US-11-004-639-44 Sequence 44, Appl
33 533.5 85.8 641 5 US-10-723-003-46 Sequence 46, Appl
34 533.5 85.8 641 6 US-11-004-639-46 Sequence 46, Appl
35 533.5 85.8 657 5 US-10-723-003-48 Sequence 48, Appl
36 533.5 85.8 657 6 US-11-004-639-48 Sequence 48, Appl
37 531.5 85.5 120 4 US-10-366-709-35 Sequence 35, Appl
38 530.5 85.3 423 4 US/10/013 Sequence 8, Appl
39 530.5 85.3 423 4 US/10/150 Sequence 8, Appl
40 530.5 85.3 423 4 US/10/244 Sequence 8, Appl
41 526.5 84.6 121 5 US-10-917-599-1 Sequence 1, Appl
42 525.5 84.5 140 3 US-09-305-928-6 Sequence 6, Appl
43 525.5 84.5 140 4 US-10-096-964-6 Sequence 6, Appl
44 525.5 84.5 140 5 US-10-956-039-6 Sequence 6, Appl
45 521 83.8 122 5 US-10-917-599-9 Sequence 9, Appl

```

## ALIGNMENTS

### RESULT 1

US-10-700-632-7

; Sequence 7, Application US/10700632

; Publication No. US20050118183A1

; GENERAL INFORMATION:

; APPLICANT: Immunogen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

; FILE OF INVENTION: LEUKEMIA USING THE SAME

; FILE REFERENCE: A8427

; CURRENT APPLICATION NUMBER: US/10/700,632

; CURRENT FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/424,332

; PRIOR FILING DATE: 2002-11-07

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-700-632-7

```

Query Match      100.0%; Score 622; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 7.7e-49;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYFGNDDISY 60

Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYFGNDDISY 60

Qy 61 NQPKFKATLTADKSSITTAQMQLSSLTSDSAVYICAREVRLRYFDVWGAGTTVTYSS 118

Db 61 NQPKFKATLTADKSSITTAQMQLSSLTSDSAVYICAREVRLRYFDVWGAGTTVTYSS 118

### RESULT 2

US-10-700-632-73

; Sequence 73, Application US/10700632

; Publication No. US20050118183A1

; GENERAL INFORMATION:

; APPLICANT: Immunogen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

; FILE OF INVENTION: LEUKEMIA USING THE SAME

; FILE REFERENCE: A8427

; CURRENT APPLICATION NUMBER: US/10/700,632

; CURRENT FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/424,332

; PRIOR FILING DATE: 2002-11-07

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 73

```
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73

Query Match      99.4%; Score 618; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8e-48;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 117
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 117

RESULT 3
US-10-700-632-9
; Sequence 9, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized My9-6 antibody heavy chain variable region
US-10-700-632-9

Query Match      98.6%; Score 613; DB 5; Length 118;
Best Local Similarity 98.3%; Pred. No. 5.1e-48;
Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 118
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGAGTTVTVS 118

RESULT 4
US-10-366-709-39
; Sequence 39, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 39
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain CA20VH amino acid sequence
US-10-366-709-39

Query Match      86.3%; Score 536.5; DB 4; Length 121;
Best Local Similarity 84.3%; Pred. No. 4.6e-41;
Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 117
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTVS 120

QY 118 S 118
Db 121 S 121

RESULT 5
US-10-013-173-6
; Sequence 6, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain
; OTHER INFORMATION: antibody-genomic streptavidin fusion
US-10-013-173-6

Query Match      85.9%; Score 534.5; DB 4; Length 412;
Best Local Similarity 85.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWVGVIYPGNDISY 60
Db 128 QVQLVQSGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPQGQLEWIGAIYPGNGDTSY 187

QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTV 116
Db 188 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGAGTTVTV 246

QY 117 SS 118
Db 247 SS 248

RESULT 6
US-10-150-762-6
; Sequence 6, Application US/10150762
```

```
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150.762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain
; OTHER INFORMATION: antibody-genomic streptavidin fusion
; US-10-150-762-6

Query Match      85.9%; Score 534.5; DB 4; Length 412;
Best Local Similarity 85.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYFGNDDISY 60
DB 128 QVQLVQSGAEELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYFGNGDTSY 187
QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 116
DB 188 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 246
QY 117 SS 118
DB 247 SS 248

RESULT 7
US-10-244-821-6
; Sequence 6, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstynne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244.821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain
; OTHER INFORMATION: antibody-genomic streptavidin fusion
; US-10-244-821-6

Query Match      85.9%; Score 534.5; DB 4; Length 412;
Best Local Similarity 85.2%; Pred. No. 2.6e-40;
Matches 104; Conservative 6; Mismatches 7; Indels 5; Gaps 2;
```

```
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYFGNDDISY 60
DB 128 QVQLVQSGAEELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYFGNGDTSY 187
QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 116
DB 188 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 246
QY 117 SS 118
DB 247 SS 248

RESULT 8
US-10-238-681-11
; Sequence 11, Application US/10238681
; Publication No. US20030147885A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: LEONARD, JOHN E.
; APPLICANT: NEWMAN, ROLAND A.
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: RASTETTER, WILLIAM H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELED
; ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; FILE REFERENCE: 37003/0291808
; CURRENT APPLICATION NUMBER: US/10/238.681
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 08/921.060
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/149.099
; PRIOR FILING DATE: 1993-11-03
; PRIOR APPLICATION NUMBER: 07/978.891
; PRIOR FILING DATE: 1992-11-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Murine sp.
; US-10-238-681-11

Query Match      85.8%; Score 533.5; DB 4; Length 140;
Best Local Similarity 83.5%; Pred. No. 1e-40;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
```

```
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYFGNDDISY 60
DB 20 QVQLQPGAEELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYFGNGDTSY 79
QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 117
DB 80 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR----YFDVWGAGTTVTY 139
QY 118 S 118
DB 140 A 140

RESULT 9
US-10-411-037-62
; Sequence 62, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFreeze, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
```

```

; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-62

Query Match      85.8%; Score 533.5; DB 4; Length 140;
Best Local Similarity 83.5%; Pred No. 1e-40;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGRLGIEWIGAIYPGNGDTSY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCARSTYYGGDWYFNWVGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 S 118
;
Db 140 A 140

RESULT 11
US-10-410-962-62
; Sequence 62, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-962-62

Query Match      85.8%; Score 533.5; DB 4; Length 140;
Best Local Similarity 83.5%; Pred No. 1e-40;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKTPGRLGIEWIGAIYPGNGDTSY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYYCARSTYYGGDWYFNWVGAGTTVTVS 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 S 118
;
Db 140 A 140

RESULT 10
US-10-411-026-62
; Sequence 62, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
```

Db 20 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 79  
QY 61 NQKFKGKATLTADKSSSTAYNQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117  
Db 80 NQKFKGKATLTADKSSSTAYNQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139  
QY 118 S 118  
Db 140 A 140

## RESULT 12

US-10-411-049-62  
; Sequence 62, Application US/10411049  
; Publication No. US20040082026A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DePrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
; FILE REFERENCE: 040853-01-5055  
; CURRENT APPLICATION NUMBER: US/10/411,049  
; PRIOR FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 62  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-411-049-62

Query Match 85.8%; Score 533.5; DB 4; Length 140;  
Best Local Similarity 83.5%; Pred. No. 1e-40;  
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 60  
Db 20 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 79  
QY 61 NQKFKGKATLTADKSSSTAYNQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117  
Db 80 NQKFKGKATLTADKSSSTAYNQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139  
QY 118 S 118  
Db 140 A 140

## RESULT 13

US-10-327-663-14  
; Sequence 14, Application US/10327663  
; Publication No. US20040093621A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenya SHITARA

; APPLICANT: Mikiko SAKURADA  
; APPLICANT: Kazuhisa UCHIDA  
; APPLICANT: Toyohisa SHINKAWA  
; APPLICANT: Mitsuo SATOH  
; APPLICANT: Ryoosuke NAKANO  
; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20  
; FILE REFERENCE: 249-289  
; CURRENT APPLICATION NUMBER: US/10/327,663  
; PRIOR FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: JP 2001-392753  
; PRIOR FILING DATE: 2001-12-25  
; PRIOR APPLICATION NUMBER: JP 2002-106948  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: JP 2002-319975  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-327-663-14

Query Match 85.8%; Score 533.5; DB 4; Length 140;  
Best Local Similarity 83.5%; Pred. No. 1e-40;  
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 60  
Db 20 QVQLQQPGAEVLKPGASVKMSCKASGYTFTSYNNHWVKQTTPGRGLEWIGAIYPGNGDTSY 79  
QY 61 NQKFKGKATLTADKSSSTAYNQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117  
Db 80 NQKFKGKATLTADKSSSTAYNQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 139  
QY 118 S 118  
Db 140 A 140

## RESULT 14

US-10-410-930-62  
; Sequence 62, Application US/10410930  
; Publication No. US20040115168A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DePrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
; FILE REFERENCE: 040853-01-5056  
; CURRENT APPLICATION NUMBER: US/10/410,930  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:59:22 ; Search time 14.0476 Seconds  
(without alignments)  
388.792 Million cell updates/sec

Title: US-10-700-632-7  
Perfect score: 622  
Sequence: 1 QVLOQPGAEVVKPGASVKM.....EVRLRYFDVWGAGTTVTVS 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /SIDSS5/ptodata/2/pubpaa/US08 NEW PUB.pep.\*  
2: /SIDSS5/ptodata/2/pubpaa/US06 NEW PUB.pep.\*  
3: /SIDSS5/ptodata/2/pubpaa/US07 NEW PUB.pep.\*  
4: /SIDSS5/ptodata/2/pubpaa/US08 NEW PUB.pep.\*  
5: /SIDSS5/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /SIDSS5/ptodata/2/pubpaa/US09 NEW PUB.pep.\*  
7: /SIDSS5/ptodata/2/pubpaa/US09 NEW PUB.pep.\*  
8: /SIDSS5/ptodata/2/pubpaa/US10 NEW PUB.pep.\*  
9: /SIDSS5/ptodata/2/pubpaa/US10 NEW PUB.pep.\*  
10: /SIDSS5/ptodata/2/pubpaa/US11 NEW PUB.pep.\*  
11: /SIDSS5/ptodata/2/pubpaa/US11 NEW PUB.pep.\*  
12: /SIDSS5/ptodata/2/pubpaa/US60 NEW PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	536.5	86.3	121	11	US-11-107-028-35 Sequence 35, Appl
2	533.5	85.8	140	10	US-11-183-218-62 Sequence 62, Appl
3	533.5	85.8	140	11	US-11-183-205-62 Sequence 62, Appl
4	533.5	85.8	451	11	US-11-124-620-5 Sequence 5, Appl
5	533.5	85.8	451	11	US-11-124-620-7 Sequence 7, Appl
6	533.5	85.8	451	11	US-11-124-620-7 Sequence 25, Appl
7	507	81.5	122	10	US-11-254-182-28 Sequence 28, Appl
8	507	81.5	122	11	US-11-120-338-7 Sequence 7, Appl
9	507	81.5	122	11	US-11-106-820-7 Sequence 7, Appl
10	507	81.5	122	11	US-11-143-077-7 Sequence 7, Appl
11	507	81.5	122	11	US-11-190-364-7 Sequence 7, Appl
12	507	81.5	122	11	US-11-147-780-7 Sequence 7, Appl
13	507	81.5	122	11	US-11-143-386-7 Sequence 7, Appl
14	507	81.5	122	11	US-11-187-364-7 Sequence 7, Appl
15	507	81.5	253	11	US-11-106-820-20 Sequence 20, Appl
16	507	81.5	253	11	US-11-190-364-18 Sequence 18, Appl
17	507	81.5	253	11	US-11-147-780-18 Sequence 18, Appl
18	503	80.9	121	11	US-11-107-028-27 Sequence 27, Appl
19	500	80.4	118	11	US-11-126-798-48 Sequence 48, Appl
20	492.5	79.2	121	11	US-11-107-028-37 Sequence 37, Appl
21	492	79.1	122	11	US-11-107-028-39 Sequence 39, Appl

22	490	78.8	118	9	US-10-507-662-30	Sequence 30, Appl
23	490	78.8	118	9	US-10-507-662-31	Sequence 31, Appl
24	488.5	78.5	133	11	US-11-069-834-2	Sequence 2, Appl
25	487	78.3	118	9	US-10-507-662-36	Sequence 36, Appl
26	480	77.2	116	9	US-10-489-866-19	Sequence 19, Appl
27	479.5	77.1	119	11	US-11-054-663-123	Sequence 123, Appl
28	479	77.0	118	9	US-10-507-662-32	Sequence 32, Appl
29	474.5	76.3	121	11	US-11-107-028-38	Sequence 38, Appl
30	474	76.2	118	9	US-10-507-662-33	Sequence 33, Appl
31	473	76.0	118	9	US-10-507-662-35	Sequence 35, Appl
32	473	76.0	118	10	US-11-297-317-2	Sequence 2, Appl
33	473	76.0	118	10	US-11-297-317-4	Sequence 4, Appl
34	472	75.9	124	9	US-10-932-334-7	Sequence 7, Appl
35	472	75.9	124	9	US-10-932-334-70	Sequence 70, Appl
36	472	75.9	143	9	US-10-932-334-52	Sequence 52, Appl
37	470	75.6	124	9	US-10-932-334-13	Sequence 13, Appl
38	468	75.2	120	9	US-10-932-334-72	Sequence 72, Appl
39	468	75.2	122	11	US-11-107-028-41	Sequence 41, Appl
40	468	75.2	123	9	US-10-932-334-87	Sequence 87, Appl
41	467	75.1	120	11	US-11-226-325-198	Sequence 198, Appl
42	467	75.1	120	11	US-11-226-325-201	Sequence 201, Appl
43	467	75.1	122	9	US-10-932-334-73	Sequence 73, Appl
44	467	75.1	139	11	US-11-226-325-4	Sequence 4, Appl
45	466.5	75.0	116	11	US-11-097-812-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-11-107-028-35  
; Sequence 35, Application US/11107028  
; Publication No. US20050276803A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAN, ANDREW C.  
; APPLICANT: GONG, QIAN  
; APPLICANT: MARTIN, FLAVIUS  
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion  
; FILE REFERENCE: P2112R1  
; CURRENT APPLICATION NUMBER: US/11/107,028  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,263  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 35  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-11-107-028-35

Query Match	86.3%	Score	536.5;	DB	11;	Length	121;
Best Local Similarity	84.3%	Pred. No.	3.4e-38;				
Matches	102;	Conservative	6;	Mismatches	10;	Indels	3;
Gaps	1;						
QY	1	QVLOQPGAEVVKPGASVKMCKASGYTFTSYIHWIKOTPGGLEWGVYVGNDDISY	60				
Db	1	QVLOQPGAEVVKPGASVKMCKASGYTFTSYIHWIKOTPGGLEWGVYVGNDDISY	60				
QY	61	NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---	117				
Db	61	NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---	117				
QY	118	S 118					
Db	121	S 121					
RESULT 2							
US-11-183-218-62							
; Sequence 62, Application US/11183218							
; Publication No. US20060088906A1							

```
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; FILE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-218-62
```

```
Query Match      85.8%; Score 533.5; DB 10; Length 140;
Best Local Similarity 83.5%; Pred. No. 6.9e-38;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDDISY 60
DB      20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYPGNGDTSY 79

QY      61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
DB      80 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYYCARSTYYGGDWYFNWVGAGTTVTVS 139

QY      118 S 118
DB      140 A 140
```

```
RESULT 3
US-11-183-205-62
; Sequence 62, Application US/11183205
; Publication No. US2006030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01
```

```
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-205-62

Query Match      85.8%; Score 533.5; DB 11; Length 140;
Best Local Similarity 83.5%; Pred. No. 6.9e-38;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY      1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWVGVIYPGNDDISY 60
DB      20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKQTPGQGLEWIGAIYPGNGDTSY 79

QY      61 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVWGAGTTVTVS 117
DB      80 NQKPKGKATLTADKSSSTAYMQLSSLTSDSAVYYCARSTYYGGDWYFNWVGAGTTVTVS 139

QY      118 S 118
DB      140 A 140

RESULT 4
US-11-124-620-5
; Sequence 5, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
```



;; PRIOR FILING DATE: 2004-03-26  
;; PRIOR APPLICATION NUMBER: US 10/672,280  
;; PRIOR FILING DATE: 2003-09-26  
;; PRIOR APPLICATION NUMBER: US 10/379,392  
;; PRIOR FILING DATE: 2003-03-03  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 5  
;; LENGTH: 451  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
;; NAME/KEY: misc feature  
;; LOCATION: (243)..(243)  
;; OTHER INFORMATION: Xaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,  
;; OTHER INFORMATION: Glutamine or Threonine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (244)..(244)  
;; OTHER INFORMATION: Xaa can be Valine, Isoleucine or Methionine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (268)..(268)  
;; OTHER INFORMATION: Xaa can be Valine, Isoleucine, Threonine or Tyrosine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (272)..(272)  
;; OTHER INFORMATION: Xaa can be Histidine, Aspartic Acid or Glutamic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (276)..(276)  
;; OTHER INFORMATION: Xaa can be Glutamic Acid or Tyrosine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (278)..(278)  
;; OTHER INFORMATION: Xaa can be Lysine or Glutamic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (301)..(301)  
;; OTHER INFORMATION: Xaa can be Asparagine or Aspartic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (302)..(302)  
;; OTHER INFORMATION: Xaa can be Serine, Alanine or Aspartic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (330)..(330)  
;; OTHER INFORMATION: Xaa can be Lysine, Glutamic Acid or Threonine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (334)..(334)  
;; OTHER INFORMATION: Xaa can be Alanine, Tyrosine, Leucine or Isoleucine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (336)..(336)  
;; OTHER INFORMATION: Xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine  
;; OTHER INFORMATION: or Glutamine  
US-11-124-620-5

Query Match 85.8%; Score 533.5; DB 11; Length 451;  
Best Local Similarity 83.5%; Pred. No. 1.9e-37;  
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;  
  
Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60  
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60  
Qy 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR---YFDVWGAGTTVTVS 117  
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYICARSTYYGCDWYFNVWGAGTTVTVS 120  
US-11-124-620-5

Qy 118 S 118  
Db 121 A 121

RESULT 5  
US-11-124-620-7  
;; Sequence 7, Application US/11124620  
;; Publication No. US20060024298A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Lazar, Gregory Alan  
;; APPLICANT: Dang, Wei  
;; APPLICANT: Desjarlais, John R.  
;; APPLICANT: Karki, Sher Bahadur  
;; APPLICANT: Vafa, Omid  
;; APPLICANT: Hayes, Robert  
;; TITLE OF INVENTION: OPTIMIZED FC VARIANTS  
;; FILE REFERENCE: A-71386-9  
;; CURRENT APPLICATION NUMBER: US/11/124,620  
;; CURRENT FILING DATE: 2005-05-05  
;; PRIOR APPLICATION NUMBER: US 60/568,440  
;; PRIOR FILING DATE: 2004-07-15  
;; PRIOR APPLICATION NUMBER: US 60/589,906  
;; PRIOR FILING DATE: 2004-07-20  
;; PRIOR APPLICATION NUMBER: US 60/627,026  
;; PRIOR FILING DATE: 2004-11-09  
;; PRIOR APPLICATION NUMBER: US 60/626,991  
;; PRIOR FILING DATE: 2004-11-10  
;; PRIOR APPLICATION NUMBER: US 60/627,774  
;; PRIOR FILING DATE: 2004-11-12  
;; PRIOR APPLICATION NUMBER: US 10/822,231  
;; PRIOR FILING DATE: 2004-03-26  
;; PRIOR APPLICATION NUMBER: US 10/672,280  
;; PRIOR FILING DATE: 2003-09-26  
;; PRIOR APPLICATION NUMBER: US 10/379,392  
;; PRIOR FILING DATE: 2003-03-03  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 7  
;; LENGTH: 451  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-124-620-7

Query Match 85.8%; Score 533.5; DB 11; Length 451;  
Best Local Similarity 83.5%; Pred. No. 1.9e-37;  
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;  
  
Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60  
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTPGQGLEWGVYIPGNDISY 60  
Qy 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR---YFDVWGAGTTVTVS 117  
Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSDSAVYICARSTYYGCDWYFNVWGAGTTVTVS 120  
Qy 118 S 118  
Db 121 A 121

RESULT 6  
US-11-208-422-25  
;; Sequence 25, Application US/11208422  
;; Publication No. US20060067930A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Adams, Camellia W.  
;; APPLICANT: Lien, Samantha  
;; APPLICANT: Lowman, Henry B.  
;; APPLICANT: Marvin, Jonathan S.  
;; APPLICANT: Meng, Yu-Ju G.  
;; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION  
;; FILE REFERENCE: P2158R1

```
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; PRIOR FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-25

Query Match      85.8%; Score 533.5; DB 11; Length 451;
Best Local Similarity 83.5%; Pred. No. 1.9e-37;
Matches 101; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVLOQPGAGELVRPGASVKMSCKASGYTFTSYNMHWKQTPRQGLEWIGAIYPGNGDTSY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 120

QY 118 S 118
;
Db 121 A 121

RESULT 7
US-11-254-182-28
; Sequence 28, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GHEE, SHANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 28
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-254-182-28

Query Match      81.5%; Score 507; DB 10; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWKQTPRQGLEWIGAIYPGNGDTSY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 120

QY 117 SS 118
;
Db 121 SS 122

RESULT 8
US-11-120-338-7
; Sequence 7, Application US/11120338
; Publication No. US20050271658A1
```

```
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALLACE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-120-338-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWKQTPRQGLEWIGAIYPGNGDTSY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 120

QY 117 SS 118
;
Db 121 SS 122

RESULT 9
US-11-106-820-7
; Sequence 7, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-820-7

Query Match      81.5%; Score 507; DB 11; Length 122;
Best Local Similarity 79.5%; Pred. No. 9.8e-36;
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWKQTPRQGLEWIGAIYPGNGDTSY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLR---YFDVWGAGTTVTY 120

QY 117 SS 118
;
Db 121 SS 122
```

RESULT 10  
 US-11-143-077-7  
 ; Sequence 7, Application US/11143077  
 ; Publication No. US20060024295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brunetta, Paul G.  
 ; TITLE OF INVENTION: METHOD FOR TREATING LUPUS  
 ; FILE REFERENCE: P2133R1  
 ; CURRENT APPLICATION NUMBER: US/11/143,077  
 ; CURRENT FILING DATE: 2005-06-02  
 ; PRIOR APPLICATION NUMBER: US 60/577,235  
 ; PRIOR FILING DATE: 2004-06-04  
 ; PRIOR APPLICATION NUMBER: US 60/517,997  
 ; PRIOR FILING DATE: 2004-10-11  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SEQ ID NO 7  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-143-077-7  
  
 Query Match 81.5%; Score 507; DB 11; Length 122;  
 Best Local Similarity 79.5%; Pred. No. 9.8e-36;  
 Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;  
  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYPCGNDISY 60  
 DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60  
  
 QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSVYFDVWGAGTTVTY 116  
 DB 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSVYFDVWGAGTTVTY 120  
  
 QY 117 SS 118  
 DB 121 SS 122  
  
 RESULT 11  
 US-11-190-364-7  
 ; Sequence 7, Application US/11190364  
 ; Publication No. US20060024300A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adams ET AL.  
 ; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof  
 ; FILE REFERENCE: P1990R3CIPI  
 ; CURRENT APPLICATION NUMBER: US/11/190,364  
 ; CURRENT FILING DATE: 2005-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/434,115  
 ; PRIOR FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: US 60/526,163  
 ; PRIOR FILING DATE: 2003-12-01  
 ; PRIOR APPLICATION NUMBER: PCT/US03/40426  
 ; PRIOR FILING DATE: 2003-12-16  
 ; PRIOR APPLICATION NUMBER: US 11/147,780  
 ; PRIOR FILING DATE: 2005-06-07  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SEQ ID NO 7  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-190-364-7  
  
 Query Match 81.5%; Score 507; DB 11; Length 122;  
 Best Local Similarity 79.5%; Pred. No. 9.8e-36;  
 Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;  
  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYPCGNDISY 60  
 DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60  
  
 QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSVYFDVWGAGTTVTY 116  
 DB 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSVYFDVWGAGTTVTY 120  
  
 QY 117 SS 118  
 DB 121 SS 122

Db 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSVYFDVWGAGTTVTY 120  
 QY 117 SS 118  
 DB 121 SS 122  
  
 RESULT 12  
 US-11-147-780-7  
 ; Sequence 7, Application US/11147780  
 ; Publication No. US20060034835A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Adams ET AL.  
 ; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof  
 ; FILE REFERENCE: P1990R3CI  
 ; CURRENT APPLICATION NUMBER: US/11/147,780  
 ; CURRENT FILING DATE: 2005-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/434,115  
 ; PRIOR FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: US 60/526,163  
 ; PRIOR FILING DATE: 2003-12-01  
 ; PRIOR APPLICATION NUMBER: PCT/US03/40426  
 ; PRIOR FILING DATE: 2003-12-16  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SEQ ID NO 7  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-147-780-7  
  
 Query Match 81.5%; Score 507; DB 11; Length 122;  
 Best Local Similarity 79.5%; Pred. No. 9.8e-36;  
 Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;  
  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYPCGNDISY 60  
 DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60  
  
 QY 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSVYFDVWGAGTTVTY 116  
 DB 61 NQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARVVYNSVYFDVWGAGTTVTY 120  
  
 QY 117 SS 118  
 DB 121 SS 122  
  
 RESULT 13  
 US-11-143-386-7  
 ; Sequence 7, Application US/11143386  
 ; Publication No. US20060051345A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FROHNA, PAUL A.  
 ; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS  
 ; FILE REFERENCE: P2134R1  
 ; CURRENT APPLICATION NUMBER: US/11/143,386  
 ; CURRENT FILING DATE: 2005-06-02  
 ; PRIOR APPLICATION NUMBER: US 60/576,993  
 ; PRIOR FILING DATE: 2004-06-04  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SEQ ID NO 7  
 ; LENGTH: 122  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-11-143-386-7  
  
 Query Match 81.5%; Score 507; DB 11; Length 122;  
 Best Local Similarity 79.5%; Pred. No. 9.8e-36;  
 Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;  
  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYPCGNDISY 60  
 DB 1 QAVLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTTPRQGLEWIGAIYFGNGDTSY 60

Qy 61 NQKFKGKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLR-----YFDVWGAGTTTTV 116  
Db 61 NQKFKGKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLR-----YFDVWGAGTTTTV 120  
Qy 117 SS 118  
Db 121 SS 122

RESULT 14  
US-11-187-364-7  
; Sequence 7, Application US/11187364  
; Publication No. US20060062787A1  
; GENERAL INFORMATION:  
; APPLICANT: Hitraya, Elena  
; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME  
; FILE REFERENCE: P2149R1  
; CURRENT APPLICATION NUMBER: US/11/187,364  
; CURRENT FILING DATE: 2005-07-21  
; PRIOR APPLICATION NUMBER: US 60/590,302  
; PRIOR FILING DATE: 2004-07-22  
; NUMBER OF SEQ ID NOS: 36  
; SEQ ID NO 7  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-187-364-7

Query Match 81.5%; Score 507; DB 11; Length 122;  
Best Local Similarity 79.5%; Pred. No. 9.8e-36;  
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60  
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGALYPGNGDTSY 60  
Qy 61 NQKFKGKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLR-----YFDVWGAGTTTTV 116  
Db 61 NQKFKGKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLR-----YFDVWGAGTTTTV 120  
Qy 117 SS 118  
Db 121 SS 122

RESULT 15  
US-11-106-820-20  
; Sequence 20, Application US/11106820  
; Publication No. US20060002930A1  
; GENERAL INFORMATION:  
; APPLICANT: BRUNETTA, PAUL G  
; APPLICANT: SEWELL, KATHRYN L.  
; TITLE OF INVENTION: Treatment of Disorders  
; FILE REFERENCE: P2102R1  
; CURRENT APPLICATION NUMBER: US/11/106,820  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,227  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/565,098  
; PRIOR FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 45  
; SEQ ID NO 20  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-11-106-820-20

Query Match 81.5%; Score 507; DB 11; Length 253;  
Best Local Similarity 79.5%; Pred. No. 1.9e-35;  
Matches 97; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPGQGLEWVGVIYPGNDISY 60  
Db 24 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGALYPGNGDTSY 83  
Qy 61 NQKFKGKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLR-----YFDVWGAGTTTTV 116  
Db 84 NQKFKGKATLTADKSTTAYMQLSSLTSDSAVYYCAREVRLR-----YFDVWGAGTTTTV 143  
Qy 117 SS 118  
Db 144 SS 145

Search completed: May 9, 2006, 02:05:58  
Job time : 15.0476 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 101.749 Seconds  
(without alignments)  
487.964 Million cell updates/sec

Title: US-10-700-632-8  
Perfect score: 581  
Sequence: 1 NIMLTQSPSSLAIVAGEKVT.....CHQYLSRFTGGGKLEIKR I13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	113	8	ADO32092 Mouse ant
2	581	100.0	114	8	ADO32146 Mouse ant
3	545	93.8	113	9	AD337184 Murine SM
4	545	93.8	113	9	AEA8701 Mouse ant
5	545	93.8	133	9	ADV92466 Mouse SM5
6	545	93.8	133	9	ADV98529 Novel chi
7	545	93.8	239	9	ADV92470 SM5-1 chi
8	545	93.8	239	9	ADV98533 Novel chi
9	545	93.8	661	9	ADV92490 FL/FC/chs
10	545	93.8	661	9	ADV98553 Novel chi
11	544	93.6	112	5	AAE29266 S. aureus
12	544	93.6	112	5	ADU39970 Antibody
13	544	93.6	116	9	AEA38741 Murine an
14	544	93.6	667	9	AEA38768 Humanized
15	543	93.5	112	5	AAE29264 S. aureus
16	543	93.5	113	8	ADO32094 Humanised
17	541	93.1	113	7	ADB97820 HEV relat
18	539	92.8	112	2	AAE54933 MAB 022 V
19	535	92.1	112	5	AAE29268 S. aureus
20	534	91.9	272	5	ABG31024 Synthetic
21	534	91.9	272	7	ADM25453 Binding d
22	534	91.9	272	7	ADM42728 Synthetic
23	534	91.9	272	9	AE95396 Mouse G28
24	534	91.9	272	9	AE94430 Mouse ant

25	527	90.7	263	2	AAW90226	Aaw90226 Anti-B7.2
26	527	90.7	268	2	AAW90222	Aaw90222 Anti-B7.2
27	527	90.7	268	2	AAW90228	Aaw90228 Anti-B7.1
28	527	90.7	273	2	AAW90224	Aaw90224 Anti-B7.1
29	527	90.7	556	2	AAW90218	Aaw90218 Bispecific
30	527	90.7	580	2	AAW90217	Aaw90217 Bispecific
31	525	90.4	144	9	ADW47080	Adw47080 Light cha
32	522	89.8	132	9	AEBO8042	Aeb08042 HLA-DR sp
33	522	89.8	238	8	ADL23052	Adl23052 Mouse/hum
34	522	89.8	238	8	ADS88793	Ads88793 A mouse/h
35	522	89.8	238	9	AEBO8041	Aeb08041 Murine/hu
36	520	89.5	113	2	AAE29215	Aar29215 LL2 Mab V
37	520	89.5	113	2	AAW27695	Aaw27695 Variable
38	520	89.5	113	7	ADC97685	Adc97685 Mouse mon
39	520	89.5	244	8	ADG17479	Adg17479 Anti-CD22
40	520	89.5	244	8	ADG17485	Adg17485 Anti-CD22
41	520	89.5	244	8	ADG17476	Adg17476 Anti-CD22
42	520	89.5	244	8	ADG17478	Adg17478 Anti-CD22
43	519	89.3	244	8	ADG17481	Adg17481 Anti-CD22
44	519	89.3	244	8	ADG17486	Adg17486 Anti-CD22
45	517	89.0	244	8	ADG17477	Adg17477 Anti-CD22

ALIGNMENTS

RESULT 1  
ADO32092  
ID ADO32092 standard; protein; 113 AA.  
XX  
AC ADO32092;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Mouse anti-CD33 antibody My9-6 light chain variable region SEQ ID NO:8.  
XX  
KW anti-CD33 antibody; epitope-binding fragment;  
KW complementarity-determining region; CDR; immunconjugate; cytostatic;  
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;  
KW light chain.  
XX  
OS Mus musculus.  
XX  
PN WO2004043344-A2.  
XX  
PD 27-MAY-2004.  
XX  
PF 05-NOV-2003; 2003WO-US032737.  
XX  
PR 07-NOV-2002; 2002US-0424332P.  
XX  
PA (IMMU-) IMMUNOGEN INC.  
XX  
PI Hoffee MG, Tavares D, Lutz RJ;  
DR WPI; 2004-411619/38.  
DR N-PSDB; ADO32139.  
XX  
XX New antibodies that bind to CD33, useful for treating a disease  
PT associated with CD33 expression, such as myelodysplastic syndrome, acute  
or chronic myeloid leukemia.  
XX  
PS Claim 8; SEQ ID NO 8; 124pp; English.  
XX  
CC The present invention describes an isolated anti-CD33 antibody or its  
epitope-binding fragment comprising: (a) at least one complementarity-  
determining region (CDR); or (b) at least heavy chain variable region  
comprising 3 CDRs, and at least one light chain variable region, where  
the CDR has the ability to bind CD33. Also described: (1) an  
immunconjugate comprising the antibody or its epitope-binding fragment  
linked to a drug or prodrug; (2) a composition comprising the antibody or  
epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical

CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment,  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents the mouse anti-CD33 antibody My9-6 light chain  
 CC variable region, which is used in an example from the present invention.  
 XX  
 SQ Sequence 113 AA;

Query Match 100.0%; Score 581; DB 8; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-39;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60  
 DB 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60  
 QY 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYYCHQYLSRRTFGGKLEIKR 113  
 DB 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYYCHQYLSRRTFGGKLEIKR 113

RESULT 2  
 AD032146  
 ID AD032146 standard; protein; 114 AA.  
 AC AD032146;  
 XX  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62.  
 XX  
 KW anti-CD33 antibody; epitope-binding fragment;  
 KW complementarity-determining region; CDR; immunoconjugate; cytostatic;  
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2004043344-A2.  
 XX  
 XX 27-MAY-2004.  
 XX  
 XX 05-NOV-2003; 2003NO-US032737.  
 XX  
 XX 07-NOV-2002; 2002US-0424332P.  
 XX  
 XX (IMMU-) IMMUNOGEN INC.  
 XX  
 XX Hoffee MG, Tavares D, Lutz RJ;  
 XX WPI; 2004-411619/38.  
 XX  
 XX New antibodies that bind to CD33, useful for treating a disease  
 XX associated with CD33 expression, such as myelodysplastic syndrome, acute

PT or chronic myeloid leukemia.  
 XX  
 XX Example 3; SEQ ID NO 62; 124pp; English.  
 CC  
 CC The present invention describes an isolated anti-CD33 antibody or its  
 CC epitope-binding fragment comprising: (a) at least one complementarity-  
 CC determining region (CDR); or (b) at least heavy chain variable region  
 CC comprising 3 CDRs, and at least one light chain variable region, where  
 CC the CDR has the ability to bind CD33. Also described: (1) an  
 CC immunoconjugate comprising the antibody or its epitope-binding fragment  
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or  
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment,  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents a mouse anti-CD33 antibody light chain homologous  
 CC amino acid sequence, which is used in an example from the present  
 CC invention.  
 XX  
 SQ Sequence 114 AA;

Query Match 100.0%; Score 581; DB 8; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-39;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60  
 DB 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNIYAWYQQIPGQSPKLLIYWASTR 60  
 QY 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYYCHQYLSRRTFGGKLEIKR 113  
 DB 61 ESGVPRDFTGSGSGTDFLTITSSVQSEDLAIYYCHQYLSRRTFGGKLEIKR 113

RESULT 3  
 ADX37184  
 ID ADX37184 standard; protein; 113 AA.  
 XX  
 XX  
 AC ADX37184;  
 XX  
 XX 21-APR-2005 (first entry)  
 XX  
 XX Murine SMS-1 antibody, mSMS-1, light chain variable region, SEQ ID 4.  
 XX  
 XX Cytostatic; Gene Therapy; light chain variable region; SMS-1; neoplasm;  
 XX melanoma; breast tumor; hepatocellular carcinoma.  
 XX  
 XX Mus musculus.  
 XX  
 XX US2005031617-A1.  
 XX  
 XX 10-FEB-2005.  
 XX  
 XX 26-NOV-2003; 2003US-00722849.

```

XX 06-JUN-2003; 2003CN-00129123.
PR 25-NOV-2003; 2003CN-01119926.
XX (MAJJ/) MA J.
XX (GUOY/) GUO Y.
XX
XX Ma J, Guo Y;
XX
XX WPI; 2005-131967/14.
DR N-PSDB; ADX37188.
XX
XX New antibody that competitively inhibits the immunospecific binding of a
PT human SMS-1 specific monoclonal antibody to a SMS-1 target antigen,
PT useful for diagnosing or treating neoplasms, e.g. melanoma or breast
PT cancer.
XX
XX Claim 11; SEQ ID NO 4; 40pp; English.
XX
XX The present invention relates to antibodies which are specific for the
CC cancer associated antigen SMS-1. The antibodies are useful for assaying
CC for SMS-1 antigen in a sample, which is useful for the prognosis or
CC diagnosis of a neoplasm, e.g. melanoma, breast cancer, or hepatocellular
CC carcinoma. The present sequence is a variable region of one such anti-SMS
CC -1 antibody.
XX
XX Sequence 113 AA;
SQ
Query Match 93.8%; Score 545; DB 9; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.3e-36;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPQSPKLLIYWASTR 60
DB 1 NIMWTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVPRFTGSGSGTFTLTISVQSEDLAIVYCHQYLSRRTGGGTKLEIKR 113
DB 61 ESGVPRFTGSGSGTFTLTISVQAEADLAIVYCHQYFSYTRGGGTKLEIKR 113
RESULT 4
AEA88701
ID AEA88701 standard; protein; 113 AA.
XX
XX AEA88701;
XX
XX 25-AUG-2005 (first entry)
XX
XX Mouse anti-SMS-1 antibody light chain variable region, SEQ ID: 4.
XX
XX cancer; cytostatic; neoplasm; melanoma; breast tumor; endocrine disease;
KW hepatocellular carcinoma; immunotherapy; light chain variable region;
KW SMS-1.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Key 24..40
FT Region /note= "Variable region"
FT Region 56..62
FT Region /note= "Variable region"
FT Region 95..102
FT Region /note= "Variable region"
XX
XX W02005053604-A2.
XX
XX 16-JUN-2005.
XX
XX 04-JUN-2004; 2004WO-US017855.
XX
XX 06-JUN-2003; 2003CN-00129123.
PR 25-NOV-2003; 2003CN-01119926.

```

```

PR 26-NOV-2003; 2003US-00722849.
XX 28-NOV-2003; 2003TW-00133571.
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
XX Ma J, Guo Y;
XX
XX WPI; 2005-435284/44.
DR N-PSDB; AEA88705.
XX
XX New antibody competitively inhibiting immunospecific binding of a human
PT SMS-1 specific monoclonal antibody to a SMS-1 target antigen, useful in
PT treating malignancies such as melanoma, breast cancer or hepatocellular
PT carcinoma.
XX
XX Claim 11; SEQ ID NO 4; 85pp; English.
XX
XX The present invention relates to an antibody that competitively inhibits
CC the immunospecific binding of a human SMS-1 specific monoclonal antibody
CC (huSMS-1) to a SMS-1 target antigen. The invention is useful in the
CC fields of cancer biology and immunotherapy, in particular for diagnosing
CC and treating malignancies such as melanoma, breast cancer or
CC hepatocellular carcinoma. The present sequence is the mouse anti-SMS-1
CC antibody light chain variable (VL) region.
XX
XX Sequence 113 AA;
SQ
Query Match 93.8%; Score 545; DB 9; Length 113;
Best Local Similarity 92.0%; Pred. No. 1.3e-36;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPQSPKLLIYWASTR 60
DB 1 NIMWTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVPRFTGSGSGTFTLTISVQSEDLAIVYCHQYLSRRTGGGTKLEIKR 113
DB 61 ESGVPRFTGSGSGTFTLTISVQAEADLAIVYCHQYFSYTRGGGTKLEIKR 113
RESULT 5
ADV92466
ID ADV92466 standard; protein; 133 AA.
XX
XX ADV92466;
XX
XX 10-MAR-2005 (first entry)
XX
XX Mouse SMS-1 (mSMS-1) light chain variable region protein.
XX
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Key 1..20
FT Peptide /note= "signal peptide"
FT Region 21..133
FT Region /note= "light chain variable region gene (VL)"
FT Protein 21..133
FT Protein /note= "Mature Mouse SMS-1 (mSMS-1) light chain variable
FT region protein"
XX
XX US2004254108-A1.
XX
XX 16-DEC-2004.
XX
XX 26-NOV-2003; 2003US-00723003.
XX
XX 13-JUN-2003; 2003CN-00129290.
PR 25-NOV-2003; 2003CN-01119930.

```

```
XX (MAJJ/) MA J.  
PA (GUOY/) GUO Y.  
XX Ma J, Guo Y;  
PI  
XX  
DR WPI; 2005-030218/03.  
DR N-PSDB; ADV92465.  
XX  
XX New chimeric protein comprises an Flt3 ligand and a proteinous or  
PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
XX  
PS Example 3; SEQ ID NO 10; 158pp; English.  
XX  
XX The present invention relates to a chimeric protein having a Flt3 ligand  
CC (FL) or its biologically active fragment and a proteinous or peptidyl  
CC tumoricidal agent. The invention is useful for treating malignancy,  
CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
CC vaccine for eliciting an immune response. The invention is also useful in  
CC gene therapy. The present sequence is the mouse SM5-1 (mSM5-1) light  
CC chain variable region protein.  
XX  
XX Sequence 133 AA;  
SQ  
Query Match 93.8%; Score 545; DB 9; Length 133;  
Best Local Similarity 92.0%; Pred. No. 1.6e-36;  
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQOIPGQSPKLLIYWASTR 60  
Db 21 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOIPGQSPKLLIYWASTR 80  
QY 61 ESGVDPDRFTGSGSGDTFTLTISVQSEDLAIVYCHOYLSRRFTGGGKLEIKR 113  
Db 81 ESGVDPDRFTGSGSGDTFTLTISVQAEADLAVVYCHQYFSSYTFGGGKLEIKR 133  
RESULT 6  
ADV98529  
ID ADV98529 standard; protein; 133 AA.  
XX  
AC ADV98529;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX Novel chimeric protein-related mSM5-1 light chain protein SeqID10.  
XX protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
XX  
XX Mus sp.  
OS  
XX WO2005001048-A2.  
PN  
XX  
XX 06-JAN-2005.  
PD  
XX  
XX 04-JUN-2004; 2004WO-US017765.  
PF  
XX  
XX 13-JUN-2003; 2003CN-00129290.  
PR  
XX 25-NOV-2003; 2003CN-01119930.  
PR  
XX 26-NOV-2003; 2003US-00723003.  
PR  
XX 28-NOV-2003; 2003TW-00133577.  
XX  
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.  
PA  
XX  
XX Ma J, Guo Y;  
PI  
XX WPI; 2005-075540/08.  
DR  
XX N-PSDB; ADV98528.  
DR  
XX New chimeric protein for preventing or treating neoplastic conditions,  
PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
```

```
PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal  
PT agent.  
XX  
XX Example 3; SEQ ID NO 10; 147pp; English.  
XX  
XX This invention relates to a novel chimeric protein comprising an Flt3  
CC ligand, or its biological fragment, and a proteinous or peptidyl  
CC tumoricidal agent. The invention may be useful for the production of  
CC compounds with a cytostatic activity or a vaccine. The composition and  
CC methods are useful for preventing or treating neoplastic conditions, such  
CC as melanoma, breast cancer or hepatocellular carcinoma. The present  
CC sequence is that of a protein which is related to the chimeric proteins  
CC of the invention.  
XX  
XX Sequence 133 AA;  
SQ  
Query Match 93.8%; Score 545; DB 9; Length 133;  
Best Local Similarity 92.0%; Pred. No. 1.6e-36;  
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQOIPGQSPKLLIYWASTR 60  
Db 21 NIMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOIPGQSPKLLIYWASTR 80  
QY 61 ESGVDPDRFTGSGSGDTFTLTISVQSEDLAIVYCHOYLSRRFTGGGKLEIKR 113  
Db 81 ESGVDPDRFTGSGSGDTFTLTISVQAEADLAVVYCHQYFSSYTFGGGKLEIKR 133  
RESULT 7  
ADV92470  
ID ADV92470 standard; protein; 239 AA.  
XX  
AC ADV92470;  
XX  
XX 10-MAR-2005 (first entry)  
XX  
XX SM5-1 chimeric antibody (ChSM) light chain protein.  
XX  
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;  
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;  
KW breast cancer; hepatocellular carcinoma.  
XX  
XX Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX  
XX Key Location/Qualifiers  
FH 1..20  
FT Peptide /label= Signal peptide  
FT 21..239 /note= "Mature SM5-1 chimeric antibody (ChSM) light chain  
FT Protein protein"  
FT 21..133 /note= "Light chain variable region gene (VL)"  
FT Region 134..239 /note= "Human kappa chain constant cDNA (CL)"  
FT Region  
FT  
XX US2004254108-A1.  
PN  
XX  
XX 16-DEC-2004.  
PD  
XX  
XX 26-NOV-2003; 2003US-00723003.  
PF  
XX  
XX 13-JUN-2003; 2003CN-00129290.  
PR  
XX 25-NOV-2003; 2003CN-01119930.  
PR  
XX  
XX (MAJJ/) MA J.  
PA (GUOY/) GUO Y.  
XX  
XX Ma J, Guo Y;  
PI  
XX WPI; 2005-030218/03.  
DR
```



DR N-PSDB; ADV92469.  
XX New chimeric protein comprises an Flt3 ligand and a proteinous or peptidyl  
PT peptidyl tumorocidal agent, useful for treating malignancy or neoplasm,  
PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.

XX Example 3; SEQ ID NO 14; 158pp; English.

XX The present invention relates to a chimeric protein having a Flt3 ligand  
CC (FL) or its biologically active fragment and a proteinous or peptidyl  
CC tumorocidal agent. The invention is useful for treating malignancy,  
CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
CC vaccine for eliciting an immune response. The invention is also useful in  
CC gene therapy. The present sequence is the SM5-1 chimeric antibody (CHSM)  
CC light chain protein.

XX Sequence 239 AA;

Query Match 93.8%; Score 545; DB 9; Length 239;  
Best Local Similarity 92.0%; Pred. No. 2.7e-36;  
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSSQKNYLAWYQOIPQSPKLLIYWASTR 60  
DB 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKQSPKLLIYWASTR 80

QY 61 ESGVPRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRTFGGKLEIKR 113  
DB 81 ESGVPRFTGSGSGTDTLTITSSVQAEADLAVYCHQYFSSYTFGGKLEIKR 133

#### RESULT 8

ADV98533  
ID ADV98533 standard; protein; 239 AA.

XX AC ADV98533;

XX 24-MAR-2005 (first entry)

XX DE Novel chimeric protein-related CHSM light chain protein SeqID14.

XX KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
XX neoplasm; melanoma; breast tumor; hepatocellular carcinoma.

XX OS Mus sp.

XX OS Synthetic.

XX PN WO200501048-A2.

XX 06-JAN-2005.

XX PF 04-JUN-2004; 2004WO-US017765.

XX 13-JUN-2003; 2003CN-00129290.

XX 25-NOV-2003; 2003CN-01119930.

XX 26-NOV-2003; 2003US-00723003.

XX 28-NOV-2003; 2003TW-00133577.

XX (SYMB-) SYMBIGENE ACQUISITION CO INC.

XX Ma J, Guo Y;

XX WPI; 2005-075540/08.

XX N-PSDB; ADV98532.

XX New chimeric protein for preventing or treating neoplastic conditions,  
XX e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an  
XX Flt3 ligand or its fragment, and a proteinous or peptidyl tumorocidal  
XX agent.

XX Example 3; Fig 9; 147pp; English.

XX This invention relates to a novel chimeric protein comprising an Flt3

CC ligand, or its biological fragment, and a proteinous or peptidyl  
CC tumorocidal agent. The invention may be useful for the production of  
CC compounds with a cytostatic activity or a vaccine. The composition and  
CC methods are useful for preventing or treating neoplastic conditions, such  
CC as melanoma, breast cancer or hepatocellular carcinoma. The present  
CC sequence is that of a protein which is related to the chimeric proteins  
CC of the invention. Note: Two sequences were allocated this SeqID number in  
CC the specification, the alternative sequence is shown on page 21.

XX Sequence 239 AA;

Query Match 93.8%; Score 545; DB 9; Length 239;  
Best Local Similarity 92.0%; Pred. No. 2.7e-36;  
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSSQKNYLAWYQOIPQSPKLLIYWASTR 60  
DB 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKQSPKLLIYWASTR 80

QY 61 ESGVPRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRTFGGKLEIKR 113

DB 81 ESGVPRFTGSGSGTDTLTITSSVQAEADLAVYCHQYFSSYTFGGKLEIKR 133

#### RESULT 9

ADV92490

ID ADV92490 standard; protein; 661 AA.

XX AC ADV92490;

XX 10-MAR-2005 (first entry)

XX FL/Fc/chSMPv fusion protein.

XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;  
XX vaccine; gastrointestinal disease; immune response; melanoma; malignancy;  
XX breast cancer; hepatocellular carcinoma.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Chimeric.

XX Key Location/Qualifiers

XX FT Peptide 1..26

XX FT /label= Signal peptide

XX FT Protein 27..661

XX FT /note= "Mature FL/Fc/chSMPv fusion protein"

XX FT Region 27..182

XX FT /note= "Flt3 ligand extracellular region (FLEX)"

XX FT Region 183..197

XX FT /note= "Hinge region"

XX FT Region 198..307

XX FT /note= "CH2 region"

XX FT Misc-difference 271

XX FT /note= "Encoded by TGC"

XX FT Region 308..414

XX FT /note= "CH3 region"

XX FT Region 415..533

XX FT /note= "Heavy chain variable region gene (VH)"

XX FT Region 534..556

XX FT /note= "Linker region"

XX FT Region 557..661

XX FT /note= "Light chain variable region gene (VL)"

XX US2004254108-A1.

XX 16-DEC-2004.

XX 26-NOV-2003; 2003US-00723003.

XX 13-JUN-2003; 2003CN-00129290.

XX 25-NOV-2003; 2003CN-01119930.

XX

PA (MAJJ/) MA J.  
 PA (GUOY/) GUO Y.  
 XX  
 PI Ma J, Guo Y;  
 XX  
 DR WPI; 2005-030218/03.  
 DR N-PSDB; ADV92489.  
 XX  
 XX New chimeric protein comprises an Flt3 ligand and a proteinous or  
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
 XX  
 PS Claim 23; SEQ ID NO 34; 158pp; English.  
 XX  
 CC The present invention relates to a chimeric protein having a Flt3 ligand  
 CC (FL) or its biologically active fragment and a proteinous or peptidyl  
 CC tumoricidal agent. The invention is useful for treating malignancy,  
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
 CC vaccine for eliciting an immune response. The invention is also useful in  
 CC gene therapy. The present sequence is the FL/Fc/chSMFv fusion protein.  
 XX  
 SQ Sequence 661 AA;  
 Query Match 93.8%; Score 545; DB 9; Length 661;  
 Best Local Similarity 92.0%; Pred. No. 7.2e-36;  
 Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKYNLAYWYQQIPGQSPKLLIYWASTR 60  
 Db 549 NIMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKYNLAYWYQQKPGQSPKLLIYWASTR 608  
 QY 61 ESGVDRFTGSGSGDTFTLTISVQSEDLAIYVCHQYLSRRTFGGTTKLEIKR 113  
 Db 609 ESGVDRFTGSGSGDTFTLTISVQAEADLAVYVCHQYFSSYTFGGTTKLEIKR 661  
 RESULT 10  
 ADV98553  
 ID ADV98553 standard; protein; 661 AA.  
 XX  
 AC ADV98553;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Novel chimeric protein-related FL/Fc/chSMFv protein SeqID34.  
 XX  
 KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO2005001048-A2.  
 XX  
 PD 06-JAN-2005.  
 XX  
 PF 04-JUN-2004; 2004WO-US017765.  
 XX  
 PR 13-JUN-2003; 2003CN-00129290.  
 PR 25-NOV-2003; 2003CN-01119930.  
 PR 26-NOV-2003; 2003US-00723003.  
 PR 28-NOV-2003; 2003TW-00133577.  
 XX  
 XX (SYMB-) SYMBIGENE ACQUISITION CO INC.  
 XX  
 XX Ma J, Guo Y;  
 PI  
 DR WPI; 2005-075540/08.  
 DR N-PSDB; ADV98552.  
 XX  
 XX New chimeric protein for preventing or treating neoplastic conditions,  
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an

PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal  
 PT agent.  
 XX  
 PS Claim 23; SEQ ID NO 34; 147pp; English.  
 XX  
 CC This invention relates to a novel chimeric protein comprising an Flt3  
 CC ligand, or its biological fragment, and a proteinous or peptidyl  
 CC tumoricidal agent. The invention may be useful for the production of  
 CC compounds with a cytostatic activity or a vaccine. The composition and  
 CC methods are useful for preventing or treating neoplastic conditions, such  
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present  
 CC sequence is that of a protein which is related to the chimeric proteins  
 CC of the invention.  
 XX  
 SQ Sequence 661 AA;  
 Query Match 93.8%; Score 545; DB 9; Length 661;  
 Best Local Similarity 92.0%; Pred. No. 7.2e-36;  
 Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKYNLAYWYQQIPGQSPKLLIYWASTR 60  
 Db 549 NIMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKYNLAYWYQQKPGQSPKLLIYWASTR 608  
 QY 61 ESGVDRFTGSGSGDTFTLTISVQSEDLAIYVCHQYLSRRTFGGTTKLEIKR 113  
 Db 609 ESGVDRFTGSGSGDTFTLTISVQAEADLAVYVCHQYFSSYTFGGTTKLEIKR 661  
 RESULT 11  
 AAE29266  
 ID AAE29266 standard; protein; 112 AA.  
 XX  
 AC AAE29266;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE S. aureus Clfa specific monoclonal antibody 12-9VLA-1 protein.  
 XX  
 KW Clumping factor A; Clfa; fibrinogen; fibrin; Clf40; Clf33; N3 protein;  
 KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;  
 KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 24. .40  
 FT /note= "CDR1"  
 FT Region 56. .62  
 FT /note= "CDR2"  
 FT Region 95. .102  
 FT /note= "CDR3"  
 XX  
 PN WO200272600-A2.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 28-JAN-2002; 2002WO-US002296.  
 XX  
 PR 26-JAN-2001; 2001US-0264072P.  
 PR 12-MAR-2001; 2001US-0274611P.  
 PR 18-JUN-2001; 2001US-0298413P.  
 PR 30-JUL-2001; 2001US-0308116P.  
 XX  
 XX (INHI-) INHIBITEX INC.  
 XX  
 XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;  
 PI  
 DR WPI; 2002-759834/82.  
 DR N-PSDB; AAD46865.  
 XX  
 XX New anti- clumping factor A (Clfa) monoclonal antibody, useful for  
 PT treating or preventing Staphylococcus aureus infection e.g. wound

PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in  
 XX a human or animal.

Claim 11; Page 35; 80pp; English.

XX The invention relates to monoclonal antibody which binds the clumping  
 CC factor A (ClfA) protein from *Staphylococcus aureus*. The anti-ClfA  
 CC monoclonal antibody is useful for treating or preventing *S. aureus*  
 CC infection in a human or animal, and for inhibiting the binding of  
 CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment  
 CC of *S. aureus* Clf40 protein, *S. aureus* Clf33 protein, or the *S. aureus* N3  
 CC protein is useful for inducing an immunological response in a human or  
 CC animal. These staphylococcal infections include wound infections, sepsis,  
 CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The  
 CC present sequence is *Staphylococcus aureus* ClfA specific monoclonal  
 CC antibody 12-9VLA-1 (variable light sequence) protein  
 XX Sequence 112 AA;

Query Match 93.6%; Score 544; DB 5; Length 112;  
 Best Local Similarity 92.9%; Pred. No. 1.6e-36;  
 Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKYLAWYQIIPQSPKLLIYWASTR 60  
 Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKYLAWYQIQKPGSPKLLIYWASTR 60  
 Qy 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIIYCHQYLSSRTFGGKLEIK 112  
 Db 61 ESGVDPDRFTGSGGTDFTLTISVQAEADLAIIYCHQYLSSYTFGGKLEIK 112

#### RESULT 12

ADU39970  
 ID ADU39970 standard; protein; 112 AA.

AC ADU39970;

XX 27-JAN-2005 (first entry)

XX Antibody TF9 light chain variable region.

XX cytostatic; gene therapy; human tissue factor; antibody engineering;  
 KW blood; coagulation; plasma; diagnosing; cancer.

XX Homo sapiens.

XX WO200404475-A2.

XX 04-NOV-2004.

XX 21-APR-2004; 2004WO-US012206.

XX 22-APR-2003; 2003US-0464363P.

XX 26-JUN-2003; 2003US-0482498P.

XX 05-APR-2004; 2004US-00816938.

XX (EURO-) EUROCELTIQUE SA.

XX (WANG/) WANG B.

XX Wang B;

XX WPI; 2004-795533/78.

XX N-PSDB; ADU39969.

XX New antibodies capable of binding to human tissue factor and do not

PT inhibit tissue factor mediated blood coagulation compared to a normal

PT plasma control, useful for diagnosing, preventing or treating cancer,  
 PT such as breast cancer.

XX Disclosure; SEQ ID NO 31; 134pp; English.

XX The invention relates to an isolated antibody capable of binding to human

CC tissue factor (TF), which does not inhibit tissue factor mediated blood  
 CC coagulation compared to a normal plasma control and can initiate an Fc-  
 CC mediated mechanism. The composition and methods are useful for  
 CC diagnosing, preventing or treating cancer, such as non-small cell lung  
 CC cancer, breast cancer, colon cancer or prostate cancer. These may also be  
 CC used in screening for agents that may treat or prevent cancer. This  
 CC sequence corresponds to the light chain variable region of an anti-human  
 CC tissue factor antibody.

XX Sequence 112 AA;

Query Match 93.6%; Score 544; DB 8; Length 112;  
 Best Local Similarity 92.9%; Pred. No. 1.6e-36;  
 Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKYLAWYQIIPQSPKLLIYWASTR 60  
 Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKYLAWYQIQKPGSPKLLIYWASTR 60  
 Qy 61 ESGVDPDRFTGSGGTDFTLTISVQSEDLAIIYCHQYLSSRTFGGKLEIK 112  
 Db 61 ESGVDPDRFTGSGGTDFTLTISVQAEADLAIIYCHQYLSSYTFGGKLEIK 112

#### RESULT 13

AEA38741

ID AEA38741 standard; protein; 116 AA.

XX AEA38741;

XX 11-AUG-2005 (first entry)

XX Murine anti-TGF-beta antibody (2G7) VL protein, SEQ ID NO: 1.

XX Monoclonal antibody; animal disease model; metastasis; cytostatic;  
 KW neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;  
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;  
 KW cancer cell proliferation inhibitor;  
 KW transforming growth factor-beta-antagonist; light chain variable region.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 24..40

FT /note= "Complementarity determining region (CDR) - L1"

FT Region 56..62

FT /note= "Complementarity determining region (CDR) - L2"

FT Region 95..102

FT /note= "Complementarity determining region (CDR) - L3"

XX WO2005050200-A2.

XX 02-JUN-2005.

XX 04-NOV-2004; 2004WO-US036651.

XX 13-NOV-2003; 2003US-0520398P.

XX 31-MAR-2004; 2004US-0557951P.

XX (GETH ) GENENTECH INC.

XX Filvaroff EH;

XX WPI; 2005-417772/42.

XX Screening compounds useful for treating tumor metastasis involves  
 PT administering a test compound to non-human animal model bearing soft  
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue  
 PT growth/bone metastasis.

XX Example 2; SEQ ID NO 1; 109pp; English.

XX The present invention relates to the screening of candidate molecules

CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment  
 CC of tumor metastasis and treatment methods using such molecules. The  
 CC screening method of the invention involves administering several test  
 CC substances to a non-human syngeneic immunocompetent animal model bearing  
 CC at least one soft tissue or bone metastasis optionally in presence of a  
 CC primary tumor, determining the effects of these test substances on the  
 CC soft tissue or bone metastasis and growth of the primary tumor and  
 CC identifying a test substance inhibiting soft tissue growth or bone  
 CC metastasis without adverse effect on the status of the primary tumor. The  
 CC invention is useful in the diagnosis and treatment of breast cancer,  
 CC colorectal cancer, liver and lung metastases, bone destruction and bone  
 CC loss. The animal models of the present invention is useful to screen  
 CC substances useful for the prophylaxis or treatment of soft tissue and/or  
 CC bone metastases which may additionally be effective in treating the  
 CC primary tumor. The present sequence is murine anti-TGF-beta antibody  
 CC (2G7) variable light chain (VL) monoclonal antibody protein.  
 XX  
 SQ Sequence 116 AA;  
 Query Match 93.6%; Score 544; DB 9; Length 116;  
 Best Local Similarity 92.0%; Pred. No. 1.7e-36;  
 Matches 104; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60  
 Db 1 DIMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNOKNYLAWYQQKPGQSPKLLIYWASTR 60  
 QY 61 ESGVDPDRFTGSGSGDFTLTITSSVQSEDLAIVYCHQYLSSRTFGGGTKLEIKR 113  
 Db 61 ESGVDPDRFTGSGSGDFTLTITSSVQAEADLAVYCHQYLSSDFTFGGGTKLEIKR 113  
 RESULT 14  
 ID AEA38768 standard; protein; 667 AA.  
 XX AEA38768;  
 AC AEA38768;  
 XX  
 DT 11-AUG-2005 (first entry)  
 XX  
 DE Humanized murine anti-TGF-beta antibody protein, chimL.chimH, SEQ: 28.  
 XX  
 KW Monoclonal antibody; animal disease model; metastasis; cytostatic;  
 KW neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;  
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;  
 KW cancer cell proliferation inhibitor;  
 KW transforming growth factor-beta-antagonist; humanized antibody;  
 KW chimeric antibody.  
 XX  
 OS Mus musculus.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 220 /label= Unknown  
 FT  
 XX  
 PN WO2005050200-A2.  
 XX  
 PD 02-JUN-2005.  
 XX  
 XX 04-NOV-2004; 2004WO-US036651.  
 XX  
 PR 13-NOV-2003; 2003US-0520398P.  
 PR 31-MAR-2004; 2004US-0557951P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Filvaroff EH;  
 PI  
 XX WPI; 2005-417772/42.  
 DR  
 XX

PT Screening compounds useful for treating tumor metastasis involves  
 PT administering a test compound to non-human animal model bearing soft  
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue  
 PT growth/bone metastasis.  
 XX  
 PS Example 2; SEQ ID NO 28; 109pp; English.  
 XX  
 CC The present invention relates to the screening of candidate molecules  
 CC [anti-transforming growth factor (TGF)-beta antibodies] for the treatment  
 CC of tumor metastasis and treatment methods using such molecules. The  
 CC screening method of the invention involves administering several test  
 CC substances to a non-human syngeneic immunocompetent animal model bearing  
 CC at least one soft tissue or bone metastasis optionally in presence of a  
 CC primary tumor, determining the effects of these test substances on the  
 CC soft tissue or bone metastasis and growth of the primary tumor and  
 CC identifying a test substance inhibiting soft tissue growth or bone  
 CC metastasis without adverse effect on the status of the primary tumor. The  
 CC invention is useful in the diagnosis and treatment of breast cancer,  
 CC colorectal cancer, liver and lung metastases, bone destruction and bone  
 CC loss. The animal models of the present invention is useful to screen  
 CC substances useful for the prophylaxis or treatment of soft tissue and/or  
 CC bone metastases which may additionally be effective in treating the  
 CC primary tumor. The present sequence is humanized murine anti-transforming  
 CC growth factor-beta (anti-TGF-beta) antibody (also referred as humanized  
 CC monoclonal antibody 2G7) chimeric protein.  
 XX  
 SQ Sequence 667 AA;  
 Query Match 93.6%; Score 544; DB 9; Length 667;  
 Best Local Similarity 92.0%; Pred. No. 8.7e-36;  
 Matches 104; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60  
 Db 1 DIMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNOKNYLAWYQQKPGQSPKLLIYWASTR 60  
 QY 61 ESGVDPDRFTGSGSGDFTLTITSSVQSEDLAIVYCHQYLSSRTFGGGTKLEIKR 113  
 Db 61 ESGVDPDRFTGSGSGDFTLTITSSVQAEADLAVYCHQYLSSDFTFGGGTKLEIKR 113  
 RESULT 15  
 ID AEA29264 standard; protein; 112 AA.  
 XX AEA29264;  
 AC AEA29264;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE S. aureus Clfa specific monoclonal antibody 13-2VLA-1 protein.  
 XX  
 KW Clumping factor A; Clfa; fibrinogen; fibrin; Clf40; Clf33; N3 protein;  
 KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;  
 KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 24..40  
 FT /note= "CDR1"  
 FT Region 56..62  
 FT /note= "CDR2"  
 FT Region 95..102  
 FT /note= "CDR3"  
 XX  
 PN WO200272600-A2.  
 XX  
 PD 19-SEP-2002.  
 XX  
 XX 28-JAN-2002; 2002WO-US002296.  
 XX  
 PR 26-JAN-2001; 2001US-0264072P.  
 PR 12-MAR-2001; 2001US-0274611P.  
 PR

```
PR 18-JUN-2001; 2001US-0298413P.
XX 30-JUL-2001; 2001US-0308116P.
XX (INH1-) INHIBITEX INC.
XX
XX PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
XX
XX WPI; 2002-759834/82.
DR N-PSDB; AAD46863.
XX
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in
PT a human or animal.
XX
XX Claim 11; Page 34; 80pp; English.
XX
XX The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 13-2VLA-1 (variable light sequence) protein
XX
XX Sequence 112 AA;
SQ
Query Match 93.5%; Score 543; DB 5; Length 112;
Best Local Similarity 92.0%; Pred. No. 1.9e-36;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFSSQKKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 NIMLTQSPSSSLAVSAGEKVTMSCKSQSVFSSQKKNYLAWYQQIPGQSPKLLIYWASTR 60
Qy 61 ESGVPRFTGSGSGTDFLTINISVQSEDLAIYYCHOYLSRRTGGGKLEIK 112
Db 61 ESGVPRFTGSGSGTDFLTINISVQSEDLAIYYCHOYLSRRTGGGKLEIK 112
```

Search completed: May 9, 2006, 01:25:28  
Job time : 101.749 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:25:51 ; Search time 17.1212 Seconds  
(without alignments)  
635.031 Million cell updates/sec

Title: US-10-700-632-8  
Perfect score: 581  
Sequence: 1 NIMLTQSPSSLAIVSAGEKVT.....CHOYLSSRTFGGKLEIKR I13  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525	90.4	111	2 G30502	Ig kappa chain V r
2	498	85.7	103	2 PH1054	Ig light chain V r
3	496	85.4	112	2 S41393	Ig kappa chain V r
4	488	84.0	112	2 S43103	Ig kappa chain V-J
5	488	84.0	133	2 PS0023	Ig kappa chain pre
6	487	83.8	118	2 PT0356	Ig kappa chain V r
7	484	83.3	138	2 S26040	Ig kappa chain pre
8	481	82.8	113	2 PT0407	Ig light chain V r
9	478	82.3	112	2 S09970	Ig kappa chain V-J
10	476	81.9	101	2 S26337	Ig light chain V r
11	476	81.9	112	2 PL0265	Ig kappa chain V r
12	473.5	81.5	134	2 PC1214	Ig kappa chain pre
13	473.5	81.5	145	2 PL0014	Ig kappa chain pre
14	472.5	81.3	240	2 S06084	Ig kappa chain pre
15	469	80.7	133	1 K4H0U1	Ig kappa chain pre
16	468.5	80.6	220	2 A31790	Ig kappa chain V r
17	463.5	79.8	113	2 S34002	Ig kappa chain V r
18	463	79.7	113	2 PT0408	Ig light chain V r
19	459.5	79.1	114	1 K4HULN	Ig kappa chain V-I
20	458.5	78.9	120	2 S51147	antibody light cha
21	457.5	78.7	113	2 PL0263	Ig kappa chain V r
22	457.5	78.7	113	2 JC2270	PL7-6 antibody lig
23	457.5	78.7	134	2 S49531	anti-Sm antibody V
24	457.5	78.7	135	2 S38807	Ig light chain V-J
25	456.5	78.6	113	2 S30520	Ig kappa chain V r
26	456.5	78.6	113	2 S34003	Ig kappa chain V r
27	455.5	78.4	113	2 A49260	antitumor monoclon
28	454.5	78.2	214	2 S68212	Ig kappa chain (Ma
29	450.5	77.5	113	2 S30523	Ig kappa chain V r

30	449	77.3	104	2 PH1102	Ig light chain V r
31	448	77.1	104	2 PH1101	Ig light chain V r
32	447.5	77.0	112	2 F30538	Ig kappa chain V r
33	446.5	76.9	112	2 E30538	Ig kappa chain V r
34	445.5	76.7	109	2 S26336	Ig light chain V r
35	445.5	76.7	114	2 S44119	Ig kappa chain V-J
36	445	76.6	104	2 PH1104	Ig light chain V r
37	445	76.6	138	2 A53261	Ig kappa chain pre
38	443.5	76.3	132	2 S46373	Ig kappa chain V-J
39	443	76.2	103	2 PH1050	Ig light chain V r
40	442	76.1	104	2 PH1103	Ig light chain V r
41	441.5	76.0	113	2 PL0264	Ig kappa chain V r
42	441.5	76.0	114	2 S44116	Ig kappa chain V-J
43	439.5	75.6	111	2 S03304	Ig kappa chain V r
44	438.5	75.5	134	1 K4HU17	Ig kappa chain pre
45	435	74.9	103	2 PH1047	Ig light chain V r

ALIGNMENTS

RESULT 1

G30502  
Ig kappa chain V region (A52) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Nov-1988 #sequence\_revision 03-Nov-1988 #text\_change 21-Jan-2000  
C;Accession: G30502  
R;Bilat, D.; Webster, D.M.; Rees, A.R.  
J. Immunol. 141, 1745-1753, 1988  
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m  
A;Reference number: A30502; MUID:88315787; PMID:2457627  
A;Accession: G30502  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-111 <EIL>  
A;Cross-references: UNIPARC:UPI0000176AF0  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 90.4%; Score 525; DB 2; Length 111;  
Best Local Similarity 90.1%; Pred. No. 3.9e-39;  
Matches 100; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVLSSQKYNLAIVYQIQSPKLIYWASTR 60  
DB 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVLSSQKYNLAIVYQIQSPKLIYWASTR 60

QY 61 ESGVPRFTGSGSGDTFTLTISVSQSEDLAIYYCHQVLSRRTFGGFKLEI 111  
DB 61 ESGVPRFTGSGSGDTFTLTISVSQSEDLAIYYCHQVLSRRTFGGFKLEI 111

RESULT 2

PH1054  
Ig light chain V region (clone 202.135) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PH1054

R;Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B  
A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1054  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA

A;Residues: 1-103 <TIL>

A;Cross-references: UNIPARC:UPI0000176AAE

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-96/Domain: immunoglobulin homology <IMM>





```
RESULT 7
S26040
Ig kappa chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
C:Accession: S26040; S78098
R:Okamoto, M.; Honjo, T.
Nucleic Acids Res. 18, 1895, 1990
A:Title: Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoantibody
A:Reference number: S09216; MUID:90245589; PMID:2336368
A:Accession: S26040
A:Molecule type: DNA
A:Residues: 1-138 <OKA>
A:Cross-references: UNIPARC:UPI00001769D0; EMBL:X51742
A:Note: the authors translated the codon AGC for residue 107 as Thr and AGT for residue
R:Okamoto, M.
submitted to the EMBL Data Library, February 1990
A:Reference number: S78098
A:Accession: S78098
A:Molecule type: DNA
A:Residues: 1-87, 'w', 89-138 <OKW>
A:Cross-references: UNIPARC:UPI0000116D53; EMBL:X51742; NID:952697; PIDN:CAA36032.1; PID
C:Genetics: 22/1
A:Introns: 22/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-138/Product: Ig kappa chain (fragment) #status predicted <WAT>
F:41-121/Domain: immunoglobulin homology <IMM>

Query Match      83.3%; Score 484; DB 2; Length 138;
Best Local Similarity 79.6%; Pred. No. 1.8e-35;
Matches 90; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy  1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKYLAWYQIQGSPKLLIYWASTR 60
Db  26 DIVMSQSPSSLTSGVGEKVTMCKSSQSLYSNNQKYLAWYQIQGSPKLLIYWASTR 85
Qy  61 ESGVDPDRFTGSGGTDTFLTISSVQSEDLAIIYCHQYLSSRTFGGKLEIKR 113
Db  86 ESGVDPDRFTGSGGTDTFLTISSVQAEGLAVYFCQYYSFLTFGAGTKLEIKR 138

RESULT 8
PT0407
Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PT0407
R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibody
A:Reference number: PT0376; MUID:91147903; PMID:1900082
A:Accession: PT0407
A:Molecule type: DNA
A:Residues: 1-113 <BEH>
A:Cross-references: UNIPARC:UPI0000176A05
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match      82.8%; Score 481; DB 2; Length 113;
Best Local Similarity 82.3%; Pred. No. 2.7e-35;
Matches 93; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy  1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKYLAWYQIQGSPKLLIYWASTR 60
Db  1 DIVISQSPSSLAIVSAGEKVTMSCKSSQSLNRSRKNYLAWYQIQGSPKLLIYWASTR 60
Qy  61 ESGVDPDRFTGSGGTDTFLTISSVQSEDLAIIYCHQYLSSRTFGGKLEIKR 113
Db  61 ECGVDPDRFTGSGGTDTFLTISSVQAEGLAVYCKQSYNLYTFGGGKLEIKR 113
```

```
RESULT 9
S09970
Ig kappa chain V-J region (4C8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: S09970
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody
A:Reference number: S09955; MUID:90269328; PMID:2347362
A:Accession: S09970
A:Molecule type: mRNA
A:Residues: 1-112 <REI>
A:Cross-references: UNIPARC:UPI0000115E69; EMBL:X51858; NID:955406; PIDN:CAA36151.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match      82.3%; Score 478; DB 2; Length 112;
Best Local Similarity 79.5%; Pred. No. 5e-35;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy  1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKYLAWYQIQGSPKLLIYWASTR 60
Db  1 DIVMSQSPSSLTSGVGEKVTMCKSSQSLYSNNQKYLAWYQIQGSPKLLIYWASTR 60
Qy  61 ESGVDPDRFTGSGGTDTFLTISSVQSEDLAIIYCHQYLSSRTFGGKLEIKR 112
Db  61 ESGVDPDRFTGSGGTDTFLTISSVQAEGLAVYFCQYYSFLTFGAGTKLEIKR 112

RESULT 10
S26337
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C:Accession: S26337; S78449
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26337
A:Molecule type: mRNA
A:Residues: 1-101 <STA>
A:Cross-references: UNIPARC:UPI00001769B0; EMBL:X59193
R:Caton, A.J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S78449
A:Accession: S78449
A:Molecule type: mRNA
A:Residues: 1-60, 'T', 62-91, 'S', 93-101 <CAT>
A:Cross-references: UNIPARC:UPI0000115F7F; EMBL:X59193; NID:952323; PIDN:CAA41903.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-88/Domain: immunoglobulin homology <IMM>

Query Match      81.9%; Score 476; DB 2; Length 101;
Best Local Similarity 90.1%; Pred. No. 6.7e-35;
Matches 91; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy  9 SSLAVSAGEKVTMSCKSSQSVFSSQKYLAWYQIQGSPKLLIYWASTRESGVDPDRF 68
Db  1 SSLAVSAGEKVTMSCKSSQSVLYSSNQKYLAWYQIQGSPKLLIYWASTRESGVDPDRF 60
Qy  69 TGSQSGTDTFLTISSVQSEDLAIIYCHQYLSSRTFGGKLEIKR 109
Db  61 IGSQSGTDTFLTISSVQAEGLAVYCHQYLSTFTFGSGTKL 101

RESULT 11
PL0265
Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)
```



R;Klobeck, H.G.; Bornkamm, G.W.; Combratio, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G.  
Nucleic Acids Res. 13, 6515-6529, 1985  
A;Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germ  
A;Reference number: A93589; MUID:86041853; PMID:2997712  
A;Accession: A01904  
A;Molecule type: DNA  
A;Residues: 1-133 <KLO>  
A;Cross-references: UNIPROT:P06313; UNIPARC:UPI000012E165; GB:Z00022; GB:X51570; NID:g33  
A;Note: the sequence was determined from the differentiated gene  
C;Genetics:  
A;Gene: GDB:IGKV  
A;Cross-references: GDB:119341; OMIM:146980  
A;Map position: 2p12-2p12  
A;Introns: 17/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>  
F;21-43/Region: framework 1  
F;36-116/Domain: immunoglobulin homology <IMM>  
F;44-60/Region: complementarity-determining 1  
F;61-75/Region: framework 2  
F;76-82/Region: complementarity-determining 2  
F;83-114/Region: framework 3  
F;115-122/Region: complementarity-determining 3  
F;123-133/Region: framework 4  
F;43-114/Disulfide bonds: #status predicted

Query Match 80.7%; Score 469; DB 1; Length 133;  
Best Local Similarity 77.0%; Pred. No. 3.6e-34;  
Matches 87; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFSSQKYLAWYQOIPQSPKLLIYWASTR 60  
Db 21 DIVMTQSPDLSAVSLGRATINCKSSQSVLYSSNNKYLAWYQOQPPKLLIYWASTR 80

Qy 61 ESGVPDRFTGSGGTDFTLTISSVQSEDLAIYYCHOYLSRTFGGKLEIKR 113  
Db 81 ESGVPDRFSGSGGTDFTLTISSLAQEDVAIYYCQYDTIPTFGGKVEIKR 133

Search completed: May 9, 2006, 01:33:51  
Job time : 17.1212 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:41 ; Search time 103.461 Seconds  
(without alignments)

770.577 Million cell updates/sec

Title: US-10-700-632-8

Perfect score: 581

Sequence: 1 NIMLTQSPSSLAIVAGEKVT.....CHOYLSRTPGGGKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05-80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	469	80.7	133	1	KV4B_HUMAN	P06313 homo sapien
2	463.5	79.8	240	1	Q52164_MOUSE	Q52164 mus musculus
3	458.5	78.9	114	1	KV4A_HUMAN	P01625 homo sapien
4	451.5	77.7	134	1	KV4C_HUMAN	P06314 homo sapien
5	447.5	77.0	255	2	Q6K805_MOUSE	Q6K805 mus musculus
6	421	72.5	121	1	KV4D_HUMAN	P06312 homo sapien
7	400.5	68.9	109	1	KV40_HUMAN	P83593 homo sapien
8	384	66.1	109	2	Q9UL78_HUMAN	Q9UL78 homo sapien
9	382	65.7	129	1	KV3L_HUMAN	P18135 homo sapien
10	376.5	64.8	114	1	KV1A_MOUSE	P01632 mus musculus
11	376	64.7	107	2	Q6P5A9_HUMAN	Q96889 homo sapien
12	374	64.4	109	1	KV3E_HUMAN	P01623 homo sapien
13	373.5	64.3	108	2	Q9UL70_HUMAN	Q9UL70 homo sapien
14	372	64.0	109	1	KV3B_HUMAN	P01620 homo sapien
15	371	63.9	129	1	KV3M_HUMAN	P18136 homo sapien
16	370	63.7	109	1	KV3D_HUMAN	P01622 homo sapien
17	370	63.7	235	2	Q6GMV9_HUMAN	Q6GMV9 homo sapien
18	367.5	63.3	136	1	KV5B_MOUSE	P01634 mus musculus
19	367.5	63.3	236	2	Q6P5S8_HUMAN	Q6P5S8 homo sapien
20	367.5	63.3	238	2	Q58BU4_MOUSE	Q58BU4 mus musculus
21	367	63.2	109	2	Q9UL85_HUMAN	Q9UL85 homo sapien
22	366.5	63.1	236	2	Q6P1L8_HUMAN	Q6P1L8 homo sapien
23	365.5	62.9	99	2	Q9JL74_MOUSE	Q9JL74 mus musculus
24	364.5	62.7	149	1	KV5A_MOUSE	P01633 mus musculus
25	363.5	62.6	108	1	KV1M_HUMAN	P01605 homo sapien
26	362.5	62.4	108	2	Q9UL79_HUMAN	Q9UL79 homo sapien
27	361	62.1	109	1	KV3G_HUMAN	P04206 homo sapien
28	360.5	62.0	236	2	Q6P1H7_HUMAN	Q6P1H7 homo sapien
29	360	62.0	107	2	Q9UL81_HUMAN	Q9UL81 homo sapien
30	360	62.0	129	1	KV3H_HUMAN	P04207 homo sapien
31	359.5	61.9	108	1	KV1V_HUMAN	P04430 homo sapien

Query Match

80.7%; Score 469; DB 1; Length 133;

RESULT 1

ID	KV4B_HUMAN	STANDARD;	PRT;	133 AA.
AC	P06313;			
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig kappa chain V-IV region JI precursor.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=86041853; PubMed=2997712;			
RA	Klobeck H.G.; Bornkamm G.W.; Combriato G.; Mocikat R.; Pohlenz H.D.;			
RA	Zachau H.G.;			
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a single germline gene."			
RL	Nucleic Acids Res. 13:6515-6529 (1985).			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	EMBL; Z00022; CAA77317.1; -; Genomic_DNA.			
DR	PIR; A01904; K4HUJ1.			
DR	HSSP; P01625; ILVE.			
DR	SMR; P06313; 21-133.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 21 133			
FT	REGION 21 43			
FT	REGION 44 60			
FT	REGION 61 75			
FT	REGION 76 82			
FT	REGION 83 114			
FT	REGION 115 122			
FT	REGION 123 132			
FT	REGION 123 132			
FT	DISULFID 43 114			
FT	NON_TER 133 133			
SQ	SEQUENCE 133 AA; 14633 MW; 5FB3953066744AF4 CRC64;			

ALIGNMENTS

32	359.5	61.9	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
33	359	61.8	109	1	KV3F_HUMAN	P01624 homo sapien
34	359	61.8	110	1	KV3P_MOUSE	P01668 mus musculus
35	359	61.8	235	2	Q6GMW0_HUMAN	O6gmw0 homo sapien
36	359	61.8	235	2	Q6PJF2_HUMAN	O6pjf2 homo sapien
37	358.5	61.7	111	1	KV3L_MOUSE	P01664 mus musculus
38	358.5	61.7	111	1	KV3R_MOUSE	P01670 mus musculus
39	358.5	61.7	240	2	Q6PIH6_HUMAN	O6pih6 homo sapien
40	355.5	61.2	111	2	Q5F217_MOUSE	O5f217 mus musculus
41	355	61.1	109	2	Q9UL86_HUMAN	Q9ul86 homo sapien
42	354.5	61.0	108	1	KV1Y_HUMAN	P80362 homo sapien
43	354.5	61.0	236	2	Q6PITS_MOUSE	O6pits homo sapien
44	354.5	61.0	238	2	Q6GJS7_HUMAN	O6gjst mus musculus
45	353	60.8	239	2	Q8NEK0_HUMAN	Q8nek0 homo sapien

Best Local Similarity 77.2%; Pred. No. 4.4e-41;  
Matches 88; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

Qy	1	NIMLTGSPSLAVSAGEKVTMSCKSSOSVFFSSOKNYLAWTCOOIQSGPKLIYWASTR	60
		:::::	
Db	21	DIVMSGPSLAVSVGEKVTMSCKSSQLSDIYSYNQNLYAWYQQFGSPKLIIYWASTR	80
		:::::	
Qy	61	ESGVPRFTGSGGTFTLTITSSVQSEDLAITYYCHQYLS-SRTFGGGTKLEIKR	113
		:::::	
Db	81	ESGVDPHFSGSGGTFTLTITSSVAEDLAITYYCOOVYNNPLYTFAGTKLDLLR	134
		:::::	

```

RESULT 3
KV4A_HUMAN
ID KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN PROTEIN SEQUENCE.
RP MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
[2]
RN SEQUENCE REVISION TO 9.
RA Salomon A.;
RP Submitted (AUG-1996) to Swiss-Prot.
RC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

```

DR	PDB; 3LVE; X-ray; @=1-114.
DR	PDB; 3LVE; X-ray; A/B=1-114.
DR	PDB; 4LVE; X-ray; A=1-114.
DR	GO; GO:0005576; C:extracellular region; NAS.
DR	GO; GO:0003823; F:antigen binding; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SMO0406; IGv; 1.
DR	PROSITE; PS00835; IG_LIKE; 1.
KW	3D-structure; Bence-Jones protein; Direct protein sequencing;
KW	Immunoglobulin domain; Immunoglobulin V region.
FT	REGION 1 23
FT	REGION 24 40
FT	REGION 41 55
FT	REGION 56 62
FT	REGION 63 94
FT	REGION 95 101
FT	REGION 102 113
FT	DISULFID 23 94
FT	NON TER 114 114
FT	STRAND 4 7

Query Match 79.8%; Score 463.5; DB 2; Length 240;

```

FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 32 35
FT STRAND 36 37
FT STRAND 39 44
FT TURN 46 47
FT STRAND 51 55
FT TURN 56 58
FT STRAND 59 60
FT TURN 62 63
FT TURN 66 67
FT STRAND 74 75
FT STRAND 76 81
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 78.9%; Score 458.5; DB 1; Length 114;
Best Local Similarity 76.3%; Pred. No. 6.3e-41;
Matches 87; Conservative 15; Mismatches 11; Indels 1; Gaps 1;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 DIVMTQSPDLSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQQKPGQPKLLIYWASTR 60

Qy 61 ESGVPRDFTGSGGTDTFTLTISVQSEDLAIIYCHQYLS--RTFGGQTKLEIKR 113
Db 61 ESGVPRDFRSGSGTDTFTLTISLSQAEDVAIVYQQYVSTPSPGQGTKEIKR 114

RESULT 4
KV4C HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
probe."
RL Nucleic Acids Res. 13:6531-6544 (1985).
[2]
RN SEQUENCE REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X02990; CAA26733.1; -; mRNA.
DR HSSP; P01625; ILVE.
DR SKR; P06314; 21-134.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.

```

```

DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134
FT REGION 21 43
FT REGION 44 60
FT REGION 61 75
FT REGION 76 82
FT REGION 83 114
FT REGION 115 121
FT REGION 122 133
FT DISULFID 43 114
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 77.7%; Score 451.5; DB 1; Length 134;
Best Local Similarity 74.6%; Pred. No. 4.2e-40;
Matches 85; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 21 DIVMTQSPDLSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQQKPGQPKLLIYWASTR 80

Qy 61 ESGVPRDFTGSGGTDTFTLTISVQSEDLAIIYCHQYLS--RTFGGQTKLEIKR 113
Db 81 ESGVPRDFRSGSGTDTFTLTISLSQAEDVAIVYQQYVSTPSPGQGTKEIKR 134

RESULT 5
Q6KB05 MOUSE PRELIMINARY; PRT; 255 AA.
ID Q6KB05 MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE SCFV B8E5 protein (Fragment).
GN Names=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments."
RL J. Biol. Chem. 279:55697-55706 (2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; IKCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR NON TER 1 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 77.0%; Score 447.5; DB 2; Length 255;
Best Local Similarity 79.3%; Pred. No. 2.4e-39;
Matches 91; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
Db 137 DIVMTQSPDLSLAVSAGEKVTMSCKSSQSVLYSSNKNYLAWYQQKPGQPKLLIYGASTR 196

Qy 61 ESGVPRDFTGSGGTDTFTLTISVQSEDLAIIYCHQYLS---HOYLSRTFGGQTKLEIK 112

```

```
Db      197 ESGVDPFRFTGSGGTDFTLTITSSVQAEDLAVVYQNDHSY--PLTFGAGTKLEIK 249

RESULT 6
KV40 HUMAN
ID   KV40 HUMAN          STANDARD;          PRT;    121 AA.
AC   P06312;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-IV region precursor (Fragment).
GN   Name=IGKV4-1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86041853; PubMed=2997712;
RA   Klobbeck H.G., Bornkaum G.W., Combriato G., Mocikat R., Pohlentz H.D.,
RA   Zachau H.G.;
RT   "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT   single germline gene.";
RL   Nucleic Acids Res. 13:6515-6529(1985).
CC   -!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC
CC   EMBL; Z00023; CAA77318.1; -; Genomic DNA.
DR   PIR; A01903; K4HU.
DR   HSP; P01625; ILVE.
DR   SMR; P06312; 21-121.
DR   Ensembl; ENSG00000153586; Homo sapiens.
DR   HGNC; HGNC:5834; IGKV4-1.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; P:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   KX Immunoglobulin domain; Immunoglobulin V region; Signal.
KW   SIGNAL
FT   CHAIN          1 20
FT   REGION         21 >121
FT   REGION         21 43
FT   REGION         44 60
FT   REGION         61 75
FT   REGION         76 82
FT   REGION         83 114
FT   REGION         115 121
FT   DISULFID       43 114
FT   NON_TER        121 121
SQ   SEQUENCE      121 AA; 13380 MW; 9586AD418BD33974 CRC64;
Query Match          72.5%; Score 421; DB 1; Length 121;
Best Local Similarity 77.0%; Pred. No. 6.8e-37;
Matches 77; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY      1 NIMLTQSPSSLAVSAGEKVTMSCKSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db      21 DIWVTQSPSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTR 80
QY      61 ESGVDPFRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLS 100
Db      81 ESGVDPFRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLS 120

RESULT 7
KV40 HUMAN
ID   KV40 HUMAN          STANDARD;          PRT;    109 AA.
AC   P83593;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-IV region STH (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Abdominal adipose tissue;
RX   MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbr.1998.8515;
RA   Olsen K.E., Sletten K., Westermarck P.;
RT   "Extended analysis of AL-amyloid protein from abdominal wall
RT   subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL   Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC   -!- FUNCTION: May play an important role in fibrillogenesis.
CC
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC
CC   SMR; P83593; 1-109.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   KX Immunoglobulin V region.
KW   Immunoglobulin domain;
FT   REGION         1 23
FT   REGION         24 40
FT   REGION         41 55
FT   REGION         56 62
FT   REGION         63 94
FT   REGION         95 101
FT   REGION         102 109
FT   DISULFID       23 94
FT   UNSURE         23 23
FT   UNSURE         94 94
FT   NON_TER        109 109
SQ   SEQUENCE      109 AA; 12060 MW; 0C4F31EA1E12A0B CRC64;
Query Match          68.9%; Score 400.5; DB 1; Length 109;
Best Local Similarity 68.8%; Pred. No. 9.3e-35;
Matches 75; Conservative 15; Mismatches 18; Indels 1; Gaps 1;

QY      1 NIMLTQSPSSLAVSAGEKVTMSCKSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db      1 DIWVTQSPSLAVSLGERATINCRSSQSVLYSSNNKNYLAWYQKPGQAPKLLFSWASTR 60
QY      61 ESGVDPFRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLS-SSTFGGK 108
Db      61 ESGVDPFRFTGSGGTDFTLTITPGLQAEADVAVYCCQYRIPYTFGGAK 109

RESULT 8
KV40 HUMAN
ID   KV40 HUMAN          PRELIMINARY;      PRT;    109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
```



OC Homo.  
 RN NCBI\_TaxID=9606;  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1373487;  
 RA Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,  
 RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;  
 RT "Human combinatorial antibody libraries to hepatitis B surface  
 antigen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8436174;  
 RA Wagner S.D., Luzzatto L.;  
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
 distributed over a large portion of the V kappa locus and do not show  
 somatic mutation.";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1552291;  
 RA Martin T., Buffy S.F., Carson D.A., Kipps T.J.;  
 RT "Evidence for somatic selection of natural autoantibodies.";  
 RL J. Exp. Med. 175:983-991(1992).  
 DR ENBL; AF035036; AAD56272.1; -; mRNA.  
 DR PIR; A30501; A30601.  
 DR PIR; A30601; A30601.  
 DR PIR; B30601; B30601.  
 DR PIR; B30601; B30607.  
 DR PIR; C30601; C30601.  
 DR PIR; C30607; C30607.  
 DR PIR; C30608; C30608.  
 DR PIR; D30601; D30601.  
 DR PIR; D30607; D30607.  
 DR PIR; D30608; D30608.  
 DR PIR; F30607; F30607.  
 DR PIR; F30608; F30608.  
 DR PIR; G30501; G30601.  
 DR PIR; G30608; G30608.  
 DR PIR; H30607; H30607.  
 DR PIR; H30608; H30608.  
 DR PIR; H4151; H4151.  
 DR PIR; I30601; I30601.  
 DR PIR; PH0963; PH0963.  
 DR PIR; PH0964; PH0964.  
 DR PIR; PH0965; PH0965.  
 DR PIR; S33988; S33988.  
 DR PIR; S34096; S34096.  
 DR HSP; P01625; 1EK3.  
 DR SMR; Q9UL78; 1-109.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR NON\_TER 109 109  
 FT NON\_TER 109 109  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;  
 Query Match 66.1%; Score 384; DB 2; Length 109;  
 Best Local Similarity 68.1%; Pred. No. 5.4e-33;  
 Matches 77; Conservative 18; Mismatches 12; Indels 6; Gaps 3;  
 QY 2 IMLTQSPSSILAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTRE 61  
 Db 2 IVLTQSPGTLSPGERATLSCRASQSV--SSS---YLAWYQKPKQAPRLIYGASSRA 56

QY 62 SGVDPDRFTSGSGTDFLTITSSVQSEDIAIYCHQYLSS-RTFGGGTKLEIKR 113  
 Db 57 TGIPIRFGSGSGTDFLTITSLRLEPEDCAVYVCCQYGGSPITFGGTTKVEIKR 109  
 RESULT 9  
 KV3L HUMAN STANDARD; PRT; 129 AA.  
 ID KV3L HUMAN AC P18135;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-III region HAH precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;  
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Autoantibody-associated kappa light chain variable region gene  
 expressed in chronic lymphocytic leukemia with little or no somatic  
 mutation. Implications for etiology and immunotherapy.";  
 RL J. Exp. Med. 167:840-852(1988).  
 CC -I- DISEASE: The protein is one of the surface immunoglobulin M  
 autoantibodies expressed in patients with chronic lymphocytic  
 leukemia.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR PIR; P0022; K3HUHA.  
 DR HSP; P01625; 1EEQ.  
 DR SMR; P18135; 21-129.  
 DR Ensembl; ENSG00000169769; Homo sapiens.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 Ig kappa chain V-III region HAH.  
 FT REGION 21 43 Framework-1.  
 FT REGION 44 55 Complementarity-determining-1.  
 FT REGION 56 70 Framework-2.  
 FT REGION 71 77 Complementarity-determining-2.  
 FT REGION 78 109 Framework-3.  
 FT REGION 110 118 Complementarity-determining-3.  
 FT REGION 119 129 UKI segment.  
 FT DISULFID 43 109 By similarity.  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3C5292772774D0 CRC64;  
 Query Match 65.7%; Score 382; DB 1; Length 129;  
 Best Local Similarity 67.3%; Pred. No. 1.1e-32;  
 Matches 76; Conservative 18; Mismatches 13; Indels 6; Gaps 3;  
 QY 2 IMLTQSPSSILAVSAGEKVTMSCKSSQSVFSSQKNYLAWYQIQGSPKLLIYWASTRE 61  
 Db 22 IVLTQSPGTLSPGERATLSCRASQSV--SSS---YLAWYQKPKQAPRLIYGASSRA 76  
 QY 62 SGVDPDRFTSGSGTDFLTITSSVQSEDIAIYCHQY-LSSRTFGGGTKLEIKR 113  
 Db 77 TGIPIRFGSGSGTDFLTITSLRLEPEDFAVYVCCQYGGTSPRTFGGTTKVEIKR 129



```

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFSSQKYNLAWYQIQGSPKLLIYWASTR 60
Dd 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SSYLWYQKPGKAPKLLIYAASL 54
Qy 61 ESGVDPDRFTGSGSGTDFLTLTSSVQSEDLAIVYCHOYLSSRTFGGKLEIKR 113
Dd 55 QSGVPSRFGSGSGTDFLTLTSSIQPEDFAIVYCOQSYSTLTFGGKVEIKR 107

RESULT 12
KV3E_HUMAN STANDARD; PRT; 109 AA.
ID -KV3E_HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR PIR; A01896; K3HUL.
DR HSP; P01625; ILVE.
DR SMR; P01623; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 64.4%; Score 374; DB 1; Length 109;
Best Local Similarity 63.7%; Pred. No. 6.3e-32;
Matches 72; Conservative 18; Mismatches 17; Indels 6; Gaps 2;

Qy 2 IMLTQSPSSSLAVSAGEKVTMSCKSSQSVFSSQKYNLAWYQIQGSPKLLIYWASTRE 61
Dd 2 IVLTQSPGTLSPGERATLSCRASQSV-----SSGYLGWYQKPGQAPRLIIYGASSRA 56
Qy 62 SGVDPDRFTGSGSGTDFLTLTSSVQSEDLAIVYCHOYLSSRTFGGKLEIKR 113
Dd 57 TGIPIRFGSGSGTDFLTLTSLRLEPEDFAIVYCOQYGLRGTFGGKVEIKR 109

RESULT 13
Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
ID Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```

```

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Grossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype."
RL J. Exp. Med. 174:1639-1652(1991).
DR EMBL; AF035044; AAD56280.1; -; mRNA.
DR PIR; PH0863; PH0863.
DR HSP; P01607; IBMW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 64.3%; Score 373.5; DB 2; Length 108;
Best Local Similarity 64.9%; Pred. No. 7e-32;
Matches 74; Conservative 17; Mismatches 16; Indels 7; Gaps 2;

Qy 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFSSQKYNLAWYQIQGSPKLLIYWASTR 60
Dd 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SNYLWYQKPGKPKLLIYAASL 54
Qy 61 ESGVDPDRFTGSGSGTDFLTLTSSVQSEDLAIVYCHOYLSSRTFGGKLEIKR 113
Dd 55 QSGVPSRFGSGSGTDFLTLTSSIQPEDFAIVYCOQYGLRGTFGGKVEIKR 108

RESULT 14
KV3B_HUMAN STANDARD; PRT; 109 AA.
ID -KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.

```

```
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01892; K3HUHI.
CC HSSP; P01625; 1LVE.
CC SMR; P01620; 1-109.
CC DR GO; GO:0005576; C:extracellular region; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.
CC DR GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC DR Immunoglobulin domain; Immunoglobulin V region; Signal.
CC FT CHAIN 1 20
CC FT REGION 21 129
CC FT REGION 21 43
CC FT REGION 44 55
CC FT REGION 56 70
CC FT REGION 71 77
CC FT REGION 78 109
CC FT REGION 110 118
CC FT REGION 119 129
CC FT DISULFID 43 109
CC FT NON_TER 129 129
CC FT By similarity.
CC KW Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin V region.
CC FT DISULFID 23 89
CC FT NON_TER 109 109
CC FT By similarity.
CC SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646PFB4 CRC64;

Query Match 64.0%; Score 372; DB 1; Length 109;
Best Local Similarity 62.8%; Pred. No. 1e-31;
Matches 71; Conservative 22; Mismatches 14; Indels 6; Gaps 2;

QY 2 IMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTRE 61
Db 2 IVLTQSPGTLSPGERATLSCRASQSV-----SNSYLAWYQQKPKQAPRLLIYGASSRA 56

QY 62 SGVDPDRFTGSGSGTDTLTITISVQSEDLAIIYCHQYLSS-RTFGGKTLEIKR 113
Db 57 TGIPDRFSGSGSGTDTLTISRLEPDAFYVYCCQYGSPPQTFGGSKVEIKR 109

RESULT 15
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; P18021; K3HUHI.
CC HSSP; P01625; 1EEQ.
CC SMR; P18136; 21-129.
CC DR Ensembl; ENSG00000169769; Homo sapiens.
CC DR GO; GO:0005576; C:extracellular region; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.
```

```
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT REGION 21 43
FT REGION 44 55
FT REGION 56 70
FT REGION 71 77
FT REGION 78 109
FT REGION 110 118
FT REGION 119 129
FT DISULFID 43 109
FT NON_TER 129 129
FT By similarity.
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;

Query Match 63.9%; Score 371; DB 1; Length 129;
Best Local Similarity 66.4%; Pred. No. 1.6e-31;
Matches 75; Conservative 18; Mismatches 14; Indels 6; Gaps 3;

QY 2 IMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSSQKNYLAWYQQIPGQSPKLLIYWASTRE 61
Db 22 IVLTQSPGTLSPGERATLSCRASQSV-----YLAWYQQKPKQAPRLLIYGASSRA 76

QY 62 SGVDPDRFTGSGSGTDTLTITISVQSEDLAIIYCHQYLSS-RTFGGKTLEIKR 113
Db 77 TGIPDRFSGSGSGTDTLTISRLEPDAFYVYCCQYGSPPQTFGGKTVEIKR 129

Search completed: May 9, 2006, 01:32:36
Job time : 103.461 secs
```

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	539	92.8	112	2	US-08-435-516-28	Sequence 28, Appl
2	520	89.5	113	2	US-08-690-102A-2	Sequence 2, Appl
3	520	89.5	113	2	US-09-127-902-2	Sequence 2, Appl
4	520	89.5	113	2	US-09-155-107-2	Sequence 2, Appl
5	520	89.5	113	4	PCT-US95-09641-2	Sequence 2, Appl
6	505	86.9	130	2	US-10-146-305-7	Sequence 7, Appl
7	503	86.6	112	1	US-07-916-098A-15	Sequence 15, Appl
8	498.5	85.8	113	4	PCT-US93-08435-4	Sequence 4, Appl
9	498	85.7	259	2	US-09-419-788-115	Sequence 115, App
10	488	84.0	114	2	US-08-929-856-66	Sequence 66, Appl
11	488	84.0	219	1	US-08-353-400-34	Sequence 34, Appl
12	488	84.0	239	1	US-08-353-400-37	Sequence 37, Appl
13	487	83.8	288	2	US-09-423-439-38	Sequence 38, Appl
14	487	83.8	673	2	US-09-423-439-32	Sequence 32, Appl
15	485.5	83.6	114	1	US-08-428-257A-76	Sequence 76, Appl
16	485.5	83.6	114	2	US-07-987-264-16	Sequence 16, Appl
17	483	83.1	113	1	US-08-690-102A-6	Sequence 6, Appl
18	483	83.1	113	2	US-09-127-902-6	Sequence 6, Appl
19	483	83.1	113	2	US-09-155-107-6	Sequence 6, Appl
20	483	83.1	113	4	PCT-US95-09641-6	Sequence 6, Appl
21	482.5	83.0	220	2	US-08-952-235-1	Sequence 1, Appl
22	482.5	83.0	220	2	US-09-669-971-1	Sequence 1, Appl
23	482	83.0	249	2	US-09-297-181-4	Sequence 4, Appl
24	481.5	82.9	113	2	US-08-483-749A-16	Sequence 16, Appl
25	480	82.6	109	1	US-08-308-494A-23	Sequence 23, Appl
26	478	82.3	132	2	US-09-627-896B-4	Sequence 4, Appl
27	478	82.3	132	2	US-09-339-596A-4	Sequence 4, Appl

```
RESULT 2
US-08-690-102A-2
; Sequence 2, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-690-102A-2

Query Match 89.5%; Score 520; DB 1; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.4e-44;
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSSSLAVSAGEKVTMSCKSSQSVLVSANHNKYNLAWYQQKPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGDTFTLTISVQSEDLAIYYCHQYLSRRTFGGGTKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGDTFTLTISRQVEDLAIYYCHQYLSRRTFGGGTKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-09-127-902-2
; Sequence 2, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA

Query Match 89.5%; Score 520; DB 2; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.4e-44;
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQLTQSPSSSLAVSAGEKVTMSCKSSQSVLVSANHNKYNLAWYQQKPGQSPKLLIYWASTR 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ESGVDPDRFTGSGGDTFTLTISVQSEDLAIYYCHQYLSRRTFGGGTKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFTGSGGDTFTLTISRQVEDLAIYYCHQYLSRRTFGGGTKLEIKR 113
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-155-107-2

Query Match 89.5%; Score 520; DB 2; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.4e-44;
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
```

Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
QY 61 ESGVDPDRFTGSGGTDFTLTSSVQSEDLAIIYCHQVLSRRTFGGKLEIKR 113  
Db 61 ESGVDPDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTFGGKLEIKR 113

## RESULT 5

PCT-US95-09641-2  
; Sequence 2, Application PC/TUS9509641  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS  
; NUMBER OF SEQUENCES: 21  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/09641  
; FILING DATE: 11-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/289,576  
; FILING DATE: 12-AUG-1994  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-09641-2

Query Match 89.5%; Score 520; DB 4; Length 113;  
Best Local Similarity 89.4%; Pred. No. 1.4e-44;  
Matches 101; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAAGENVMTSCSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
QY 61 ESGVDPDRFTGSGGTDFTLTSSVQSEDLAIIYCHQVLSRRTFGGKLEIKR 113  
Db 61 ESGVDPDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTFGGKLEIKR 113

## RESULT 6

US-10-146-305-7  
; Sequence 7, Application US/10146305  
; Patent No. 6939956  
; GENERAL INFORMATION:  
; APPLICANT: YUHAN CORPORATION  
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV  
; TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME  
; FILE REFERENCE: OVI7440  
; CURRENT APPLICATION NUMBER: US/10/146,305  
; CURRENT FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: KR 10-2001-26634  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 7  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-146-305-7

Query Match 86.9%; Score 505; DB 2; Length 130;  
Best Local Similarity 84.1%; Pred. No. 5.1e-43;  
Matches 95; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAAGENVMTSCSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
QY 61 ESGVDPDRFTGSGGTDFTLTSSVQSEDLAIIYCHQVLSRRTFGGKLEIKR 113  
Db 61 ESGVDPDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTFGGKLEIKR 113

## RESULT 7

US-07-916-098A-15  
; Sequence 15, Application US/07916098A  
; Patent No. 5871732  
; GENERAL INFORMATION:  
; APPLICANT: BURKLY, LINDA C.  
; APPLICANT: CHISHOLM, PATRICIA L.  
; APPLICANT: THOMAS, DAVID W.  
; APPLICANT: ROSA, MARGARET D.  
; APPLICANT: ROSA, JOSEPH J.  
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: ALLEGRETTI & WITCOFF, LTD.  
; STREET: 10 SOUTH WACKER DRIVE  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: U.S.A.  
; ZIP: 60606  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/916,098A  
; FILING DATE: July 24, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/08843  
; FILING DATE: No. 5871732ember 27, 1991  
; CLASSIFICATION: 424  
; APPLICATION NUMBER: 07/618,542  
; FILING DATE: No. 5871732ember 27, 1990  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JOHN J. MC DONNELL  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92.310-G  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 715-1000  
; TELEFAX: (312) 715-1234  
; TELEX: 910/221-5317  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-916-098A-15

Query Match 86.6%; Score 503; DB 1; Length 112;  
Best Local Similarity 84.8%; Pred. No. 6.8e-43;  
Matches 95; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAAGENVMTSCSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
Db 1 DIQLTQSPSSLAAGENVMTSCSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
QY 61 ESGVDPDRFTGSGGTDFTLTSSVQSEDLAIIYCHQVLSRRTFGGKLEIKR 112  
Db 61 ESGVDPDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRRTFGGKLEIKR 112





```
; MOLECULE TYPE: protein
US-08-929-856-66

Query Match      84.0%; Score 488; DB 2; Length 114;
Best Local Similarity 83.2%; Pred. No. 2.2e-41;
Matches 94; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMSQSPSSLAIVSAGEKVTMSCKSSQSLNSTRKNFLAWYQQKPGSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 ESGVPRFTGSGGTDTFTLTSSVQSEDIAIYYCHVLSRRTGGGKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVPRFTGSGGTDTFTLTSSVQSEDIAIYYCHVLSRRTGGGKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-08-353-400-34
; Sequence 34, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-34

Query Match      84.0%; Score 488; DB 1; Length 219;
Best Local Similarity 84.1%; Pred. No. 4.6e-41;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMSQSPSSLAIVSAGEKVTMSCKSSQSLNSTRKNFLAWYQQKPGSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 ESGVPRFTGSGGTDTFTLTSSVQSEDIAIYYCHVLSRRTGGGKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 TSGVPRFTGSGGTDTFTLTSSVQSEDIAIYYCHVLSRRTGGGKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-08-353-400-37
; Sequence 37, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-37

Query Match      84.0%; Score 488; DB 1; Length 239;
Best Local Similarity 84.1%; Pred. No. 5.1e-41;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPQSPKLLIYWASTR 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIVMSQSPSSLAIVSAGEKVTMSCKSSQSLNSTRKNFLAWYQQKPGSPKLLIYWASTR 80
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 ESGVPRFTGSGGTDTFTLTSSVQSEDIAIYYCHVLSRRTGGGKLEIKR 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 TSGVPRFTGSGGTDTFTLTSSVQSEDIAIYYCHVLSRRTGGGKLEIKR 133
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NOV-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38
```



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:57:07 ; Search time 84.8723 Seconds  
(without alignments)  
556.303 Million cell updates/sec

Title: US-10-700-632-8  
Perfect score: 581  
Sequence: 1 NIMLTQSPSSLAIVSAGEKVT.....CHOYLSRRTFGGKLEIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_applications\_AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	113	5	US-10-700-632-8
2	581	100.0	114	5	US-10-700-632-62
3	545	93.8	113	5	US-10-722-849-4
4	545	93.8	113	6	US-11-004-659-4
5	545	93.8	113	5	US-10-723-003-10
6	545	93.8	113	6	US-11-004-639-10
7	545	93.8	239	5	US-10-723-003-14
8	545	93.8	239	6	US-11-004-639-14
9	545	93.8	661	5	US-10-723-003-34
10	545	93.8	661	6	US-11-004-639-34
11	544	93.6	112	4	US-10-056-052-10
12	544	93.6	112	5	US-10-816-938-31
13	543	93.5	112	4	US-10-056-052-6
14	543	93.5	113	5	US-10-700-632-10
15	539	92.8	112	4	US-10-229-335-28
16	535	92.1	112	4	US-10-056-052-14
17	534	91.9	272	4	US-10-207-655-14
18	534	91.9	272	4	US-10-053-530-14
19	534	91.9	272	6	US-11-089-511-14
20	534	91.9	272	6	US-11-089-190-14
21	534	91.9	272	6	US-11-088-570-14
22	534	91.9	272	6	US-11-088-737-14
23	534	91.9	272	6	US-11-088-569-14
24	534	91.9	272	6	US-11-088-693-14
25	534	91.9	272	6	US-11-089-367-14
26	534	91.9	272	6	US-11-089-368-14
27	522	89.8	132	6	US-11-013-537-2

28	522	89.8	238	6	US-11-013-537-1	Sequence 1, Appli
29	520	89.5	113	3	US-09-741-843-2	Sequence 2, Appli
30	520	89.5	113	3	US-09-894-839-2	Sequence 2, Appli
31	520	89.5	113	3	US-09-988-013A-2	Sequence 2, Appli
32	520	89.5	113	4	US-10-446-689-2	Sequence 2, Appli
33	520	89.5	113	5	US-10-787-378-2	Sequence 2, Appli
34	520	89.5	113	5	US-10-974-678-2	Sequence 2, Appli
35	516	88.8	112	4	US-10-056-052-18	Sequence 18, Appl
36	513	88.3	238	4	US-10-467-253-14	Sequence 14, Appl
37	508	87.4	112	4	US-10-467-253-7	Sequence 7, Appli
38	505	86.9	130	4	US-10-146-305-7	Sequence 7, Appli
39	495.5	85.3	146	5	US-10-830-899-56	Sequence 56, Appl
40	495.5	85.3	146	5	US-10-830-899-63	Sequence 63, Appl
41	495.5	85.3	146	5	US-10-861-662-56	Sequence 56, Appl
42	495.5	85.3	146	5	US-10-861-662-63	Sequence 63, Appl
43	485.5	83.6	114	3	US-09-749-831-16	Sequence 16, Appl
44	485	83.5	99	5	US-10-700-632-60	Sequence 60, Appl
45	482.5	83.0	220	3	US-09-995-693-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-10-700-632-8  
; Sequence 8, Application US/10700632  
; Publication No. US20050118183A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunogen, Inc.  
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID  
; FILE REFERENCE: A8427  
; CURRENT APPLICATION NUMBER: US/10/700,632  
; CURRENT FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 60/424,332  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-700-632-8

Query Match	100.0%	Score 581;	DB 5;	Length 113;
Best Local Similarity	100.0%	Pred. No. 1.7e-44;	Mismatches 0;	Indels 0;
Matches 113;	Conservative 0;			Gaps 0;
QY	1	NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR	60	
Db	1	NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR	60	
QY	61	ESGVPRFTGSGSGTFTLTISVSQSEDLAIYYCHOYLSRRTFGGKLEIKR	113	
Db	61	ESGVPRFTGSGSGTFTLTISVSQSEDLAIYYCHOYLSRRTFGGKLEIKR	113	
RESULT 2				
US-10-700-632-62				
; Sequence 62, Application US/10700632				
; Publication No. US20050118183A1				
GENERAL INFORMATION:				
APPLICANT: Immunogen, Inc.				
TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID				
FILE REFERENCE: A8427				
CURRENT APPLICATION NUMBER: US/10/700,632				
CURRENT FILING DATE: 2003-11-05				
PRIOR APPLICATION NUMBER: US 60/424,332				
PRIOR FILING DATE: 2002-11-07				
NUMBER OF SEQ ID NOS: 94				
SOFTWARE: PatentIn version 3.2				
SEQ ID NO 62				

```
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-62

Query Match      100.0%; Score 581; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
DB 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
QY 61 ESGVDPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLLSSRTFGGTTKLEIKR 113
DB 61 ESGVDPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLLSSRTFGGTTKLEIKR 113

RESULT 3
US-10-722-849-4
; Sequence 4, Application US/10722849
; Publication No. US20050031617A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; TITLE OF INVENTION: ASSOCIATED ANTIGEN SMS-1 AND USES THEREOF
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/10/722,849
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-722-849-4

Query Match      93.8%; Score 545; DB 5; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.9e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
DB 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVDPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLLSSRTFGGTTKLEIKR 113
DB 61 ESGVDPDRFTGSGGTDFTLTITSSVQAEADLAIVYCHQYFSSYTFGGTTKLEIKR 113

RESULT 4
US-11-004-659-4
; Sequence 4, Application US/11004659
; Publication No. US20050232926A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; TITLE OF INVENTION: ASSOCIATED ANTIGEN SMS-1 AND USES THEREOF
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/11/004,659
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/722,849
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113

; TYPE: PRT
; ORGANISM: Mus Musculus
US-11-004-659-4

Query Match      93.8%; Score 545; DB 6; Length 113;
Best Local Similarity 92.0%; Pred. No. 2.9e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
DB 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 80
QY 61 ESGVDPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLLSSRTFGGTTKLEIKR 113
DB 61 ESGVDPDRFTGSGGTDFTLTITSSVQAEADLAIVYCHQYFSSYTFGGTTKLEIKR 133

RESULT 5
US-10-723-003-10
; Sequence 10, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-723-003-10

Query Match      93.8%; Score 545; DB 5; Length 133;
Best Local Similarity 92.0%; Pred. No. 3.4e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR 60
DB 21 NIMLTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTR 80
QY 61 ESGVDPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLLSSRTFGGTTKLEIKR 113
DB 81 ESGVDPDRFTGSGGTDFTLTITSSVQAEADLAIVYCHQYFSSYTFGGTTKLEIKR 133

RESULT 6
US-11-004-639-10
; Sequence 10, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-004-639-10

Query Match      93.8%; Score 545; DB 6; Length 133;
Best Local Similarity 92.0%; Pred. No. 3.4e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOIPQSPKLLIYWASTR 60
Db 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKPGQSPKLLIYWASTR 80
Qy 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113
Db 81 ESGVPRFTGSGSGTDFTLTISVQAEADLAVIYCHQYFSSYTFGGGKLEIKR 133

RESULT 7
US-10-723-003-14
; Sequence 14, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-14

Query Match      93.8%; Score 545; DB 5; Length 239;
Best Local Similarity 92.0%; Pred. No. 6.2e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOIPQSPKLLIYWASTR 60
Db 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKPGQSPKLLIYWASTR 80
Qy 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113
Db 81 ESGVPRFTGSGSGTDFTLTISVQAEADLAVIYCHQYFSSYTFGGGKLEIKR 133

RESULT 8
US-11-004-639-14
; Sequence 14, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
```

```
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-14

Query Match      93.8%; Score 545; DB 6; Length 239;
Best Local Similarity 92.0%; Pred. No. 6.2e-41;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOIPQSPKLLIYWASTR 60
Db 21 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKPGQSPKLLIYWASTR 80
Qy 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113
Db 81 ESGVPRFTGSGSGTDFTLTISVQAEADLAVIYCHQYFSSYTFGGGKLEIKR 133

RESULT 9
US-10-723-003-34
; Sequence 34, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-34

Query Match      93.8%; Score 545; DB 5; Length 661;
Best Local Similarity 92.0%; Pred. No. 1.7e-40;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NIMLTQSPSSLAIVSAGEKVTMSCKSSQSVFFSSQKKNYLAWYQOIPQSPKLLIYWASTR 60
Db 549 NIMMTQSPSSLAIVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOQKPGQSPKLLIYWASTR 608
Qy 61 ESGVPRFTGSGSGTDFTLTISVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113
Db 609 ESGVPRFTGSGSGTDFTLTISVQAEADLAVIYCHQYFSSYTFGGGKLEIKR 661

RESULT 10
US-11-004-639-34
; Sequence 34, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
```

```
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 031101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; FEATURE:
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-34
```

```
Query Match          93.8%; Score 545; DB 6; Length 661;
Best Local Similarity 92.0%; Pred. No. 1.7e-40;
Matches 104; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 549 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 608

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLSRRTFGGTTKLEIK 113
Db 609 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVCHQYLSRRTFGGTTKLEIKR 661
```

```
RESULT 11
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10
```

```
Query Match          93.6%; Score 544; DB 4; Length 112;
Best Local Similarity 92.9%; Pred. No. 3.6e-41;
Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLSRRTFGGTTKLEIK 112
```

```
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVCHQYLSRRTFGGTTKLEIK 112

RESULT 12
US-10-816-938-31
; Sequence 31, Application US/10816938
; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861.1670002
; CURRENT APPLICATION NUMBER: US/10/816,938
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-816-938-31
```

```
Query Match          93.6%; Score 544; DB 5; Length 112;
Best Local Similarity 92.9%; Pred. No. 3.6e-41;
Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQSEDLAIVYCHQYLSRRTFGGTTKLEIK 112
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVCHQYLSRRTFGGTTKLEIK 112
```

```
RESULT 13
US-10-056-052-6
; Sequence 6, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-6
```

```
Query Match          93.5%; Score 543; DB 4; Length 112;
Best Local Similarity 92.0%; Pred. No. 4.4e-41;
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSQKQNYLAWYQQIPGQSPKLLIYWASTR 60
Db 1 NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKQNYLAWYQQKPGQSPKLLIYWASTR 60
```

Qy 61 ESGVDRFTGSGSGTDFLTITSSVQSEDLAIIYCHYLSSRTFGGKLEIK 112  
Db 61 ESGVDRFTGSGSGTDFLTITSSVQSEDLAIIYCHYLSSRTFGGKLEIK 112

## RESULT 14

US-10-700-632-10  
; Sequence 10, Application US/10700632  
; Publication No. US20050118183A1  
; GENERAL INFORMATION:  
; APPLICANT: ImmunoGen, Inc.  
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID  
; FILE REFERENCE: A8427  
; CURRENT APPLICATION NUMBER: US/10/700,632  
; PRIOR FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 60/424,332  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized My9-6 antibody light chain variable region  
US-10-700-632-10

Query Match 93.5%; Score 543; DB 5; Length 113;  
Best Local Similarity 93.8%; Pred. No. 4.4e-41;  
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQIQPGSPKLLIYWASTRE 61  
Db 2 IVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSQKNYLAWYQIQPGSPRELLIYWASTRE 61  
Qy 62 SGVPDRFTGSGSGTDFLTITSSVQSEDLAIIYCHYLSSRTFGGKLEIKR 113  
Db 62 SGVPDRFTGSGSGTDFLTITSSVQSEDLAIIYCHYLSSRTFGGKLEIKR 113

## RESULT 15

US-10-229-335-28  
; Sequence 28, Application US/10229335  
; Publication No. US2003014483A1  
; GENERAL INFORMATION:  
; APPLICANT: MEDAREX, INC.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR  
; IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
; NUMBER OF SEQUENCES: 28  
; STREET: P.O. Box 953, 1545 Route 22 East  
; CITY: Annandale  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08801  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/229,335  
; FILING DATE: 26-Aug-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,516  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MX1-013  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-10-229-335-28

Query Match 92.8%; Score 539; DB 4; Length 112;  
Best Local Similarity 92.0%; Pred. No. 1e-40;  
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 NIMLTQSPSSLAVSAGEKVTMSCKSSQSVFFSSQKNYLAWYQIQPGSPKLLIYWASTR 60  
Db 1 NIVMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQIQPGSPKLLIYWASTR 60  
Qy 61 ESGVDRFTGSGSGTDFLTITSSVQSEDLAIIYCHYLSSRTFGGKLEIK 112  
Db 61 ESGVDRFTGSGSGTDFLTITSSVQSEDLAIIYCHYLSSRTFGGKLEIK 112

Search completed: May 9, 2006, 02:04:58  
Job time : 84.8723 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:59:22 ; Search time 13.4524 Seconds  
(without alignments)  
388.792 Million cell updates/sec

Title: US-10-700-632-8  
Perfect score: 581  
Sequence: 1 NIMLTQSPSSLAWSAGEKVT.....CHOYLSRTSGGKLEIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /SIDSS5/ptodata/2/pubpaa/US08 NEW PUB.pep.\*  
2: /SIDSS5/ptodata/2/pubpaa/US06 NEW PUB.pep.\*  
3: /SIDSS5/ptodata/2/pubpaa/US07 NEW PUB.pep.\*  
4: /SIDSS5/ptodata/2/pubpaa/US08 NEW PUB.pep.\*  
5: /SIDSS5/ptodata/2/pubpaa/FCT\_NEW PUB.pep.\*  
6: /SIDSS5/ptodata/2/pubpaa/US09 NEW PUB.pep.\*  
7: /SIDSS5/ptodata/2/pubpaa/US10 NEW PUB.pep.\*  
8: /SIDSS5/ptodata/2/pubpaa/US10 NEW PUB.pep.\*  
9: /SIDSS5/ptodata/2/pubpaa/US10 NEW PUB.pep.\*  
10: /SIDSS5/ptodata/2/pubpaa/US11 NEW PUB.pep.\*  
11: /SIDSS5/ptodata/2/pubpaa/US11 NEW PUB.pep.\*  
12: /SIDSS5/ptodata/2/pubpaa/US60 NEW PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	544	93.6	112	11	US-11-136-559-10
2	544	93.6	116	9	US-10-981-356A-1
3	544	93.6	116	11	US-11-096-046-1
4	544	93.6	666	9	US-10-981-356A-29
5	544	93.6	667	11	US-11-096-046-29
6	543	93.5	112	11	US-11-136-559-6
7	535	92.1	112	11	US-11-136-559-14
8	531	91.4	112	11	US-11-136-559-22
9	516	88.8	112	11	US-11-136-559-18
10	491.5	84.6	259	9	US-10-512-184-31
11	491.5	84.6	329	9	US-10-512-184-68
12	479.5	82.5	329	9	US-10-512-184-33
13	479.5	82.5	329	9	US-10-512-184-70
14	474.5	81.7	113	10	US-11-219-563-71
15	474.5	81.7	113	10	US-11-219-563-91
16	474.5	81.7	113	11	US-11-218-813-71
17	474.5	81.7	113	11	US-11-218-813-91
18	470.5	81.0	114	11	US-11-127-677-27
19	469	80.7	133	8	US-10-511-937-2965
20	468	80.6	116	9	US-10-981-356A-3
21	468	80.6	116	11	US-11-096-046-3

22	468	80.6	666	9	US-10-981-356A-25	Sequence 25, Appl
23	468	80.6	666	9	US-10-981-356A-27	Sequence 27, Appl
24	468	80.6	666	9	US-10-981-356A-28	Sequence 28, Appl
25	468	80.6	666	11	US-11-096-046-27	Sequence 27, Appl
26	468	80.6	667	11	US-11-096-046-25	Sequence 25, Appl
27	468	80.6	667	11	US-11-096-046-28	Sequence 28, Appl
28	468	80.6	692	9	US-10-981-356A-26	Sequence 26, Appl
29	468	80.6	695	11	US-11-096-046-26	Sequence 26, Appl
30	463.5	79.8	259	9	US-10-512-184-34	Sequence 34, Appl
31	463.5	79.8	371	9	US-10-512-184-71	Sequence 71, Appl
32	463.5	79.8	626	9	US-10-512-184-49	Sequence 49, Appl
33	462.5	79.6	678	11	US-11-202-507A-11	Sequence 11, Appl
34	462.5	79.6	679	11	US-11-202-507A-5	Sequence 5, Appl
35	460	79.2	115	9	US-10-771-257-27	Sequence 27, Appl
36	459.5	79.1	114	9	US-10-834-397-17	Sequence 17, Appl
37	455.5	78.4	293	11	US-11-116-939-10	Sequence 10, Appl
38	455.5	78.4	412	11	US-11-116-939-12	Sequence 12, Appl
39	455.5	78.4	824	11	US-11-116-939-11	Sequence 11, Appl
40	454.5	78.2	242	11	US-11-239-510-23	Sequence 23, Appl
41	454.5	78.2	244	11	US-11-239-510-13	Sequence 13, Appl
42	454.5	78.2	483	11	US-11-239-510-19	Sequence 19, Appl
43	452.5	77.9	118	10	US-11-075-891-26	Sequence 26, Appl
44	451.5	77.7	113	11	US-11-076-395-46	Sequence 46, Appl
45	451.5	77.7	114	9	US-10-771-257-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1  
US-11-136-559-10  
; Sequence 10, Application US/11136559  
; Publication No. US20050287164A1  
; GENERAL INFORMATION:  
; APPLICANT: PATI, Joseph M  
; APPLICANT: HUTCHINS, Jeff T  
; APPLICANT: DOMANSKI, Paul  
; APPLICANT: PATEL, Pratiksha  
; APPLICANT: HALL, Andrea  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .  
; FILE REFERENCE: P07069US04/BAS  
; CURRENT APPLICATION NUMBER: US/11/136,559  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/056,052  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/308,116  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/298,413  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/274,611  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: 60/264,072  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-136-559-10

Query Match	93.6%	Score	544	DB	11	Length	112
Best Local Similarity	92.9%	Pred. No.	2.5e-33				
Matches	104	Conservative	5	Mismatches	3	Indels	0
Gaps	0						
QY	1	NIMLTQSPSSLAWSAGEKVTMTCKSSQSVFFSSQKNYLAWYQQIPGQSPKLLIYWASTR	60				
Db	1	NIMWTQSPSSLAWSAGEKVTMTCKSSQSVLYSSNQKNYLAWYQQKPGSPKLLIYWASTR	60				
QY	61	ESGVPRFTGSGSGTDTLTITSSVQSEDAIYYCHQYLSRRTFGGKLEIK	112				
Db	61	ESGVPRFTGSGSGTDTLTITSSVQSEDAIYYCHQYLSRRTFGGKLEIK	112				



QY 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113  
Db 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIKR 113

## RESULT 6

US-11-136-559-6

; Sequence 6, Application US/11136559  
; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M

; APPLICANT: HUTCHINS, Jeff T

; APPLICANT: DOMANSKI, Paul

; APPLICANT: PATEL, Pratiksha

; APPLICANT: HALL, Andrea

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

; FILE REFERENCE: P07069US04/BAS

; CURRENT APPLICATION NUMBER: US/11/136,559

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US/10/056,052

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: 60/308,116

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/298,413

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: 60/274,611

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: 60/264,072

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 6

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-11-136-559-6

Query Match 93.5%; Score 543; DB 11; Length 112;  
Best Local Similarity 92.0%; Pred. No. 3e-33;  
Matches 103; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKXNYLAWYQQIPGQSPKLLIYWASTR 60

Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKXNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIK 112

Db 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIK 112

## RESULT 7

US-11-136-559-14

; Sequence 14, Application US/11136559

; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M

; APPLICANT: HUTCHINS, Jeff T

; APPLICANT: DOMANSKI, Paul

; APPLICANT: PATEL, Pratiksha

; APPLICANT: HALL, Andrea

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

; FILE REFERENCE: P07069US04/BAS

; CURRENT APPLICATION NUMBER: US/11/136,559

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US/10/056,052

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: 60/308,116

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/298,413

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: 60/274,611

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: 60/264,072

; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 14  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-136-559-14

Query Match 92.1%; Score 535; DB 11; Length 112;  
Best Local Similarity 91.1%; Pred. No. 1.1e-32;  
Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKXNYLAWYQQIPGQSPKLLIYWASTR 60

Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKXNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIK 112

Db 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIK 112

## RESULT 8

US-11-136-559-22

; Sequence 22, Application US/11136559

; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M

; APPLICANT: HUTCHINS, Jeff T

; APPLICANT: DOMANSKI, Paul

; APPLICANT: PATEL, Pratiksha

; APPLICANT: HALL, Andrea

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .

; FILE REFERENCE: P07069US04/BAS

; CURRENT APPLICATION NUMBER: US/11/136,559

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US/10/056,052

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: 60/308,116

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/298,413

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: 60/274,611

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: 60/264,072

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 22

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-11-136-559-22

Query Match 91.4%; Score 531; DB 11; Length 112;  
Best Local Similarity 91.1%; Pred. No. 2.2e-32;  
Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIMLTQSPSSLAIVSAGEKVTMSCKSQSVFFSSQKXNYLAWYQQIPGQSPKLLIYWASTR 60

Db 1 NIMMTQSPSSLAIVSAGEKVTMSCKSQSVLYSSNQKXNYLAWYQQKPGQSPKLLIYWASTR 60

QY 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIK 112

Db 61 ESGVDRFTGSGSGTDTLTITSSVQSEDLAIIYCHQYLSRRTFGGKLEIK 112

## RESULT 9

US-11-136-559-18

; Sequence 18, Application US/11136559

; Publication No. US20050287164A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M





**THIS PAGE BLANK (uspto)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 106.251 Seconds  
(without alignments)  
487.964 Million cell updates/sec

Title: US-10-700-632-9  
Perfect score: 623  
Sequence: 1 QVQLQQPGAEVVRKPGASVRK.....EVLRLYFDVWGQTTVTVSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*  
9: Geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623	100.0	118	8 ADO32093	Ado32093 Humanised
2	613	98.4	118	8 ADO32091	Ado32091 Mouse ant
3	609	97.8	117	8 ADO32157	Ado32157 Mouse ant
4	538.5	86.4	121	7 ADJ94605	Adj94605 Chimeric
5	538.5	86.4	121	7 ADJ94607	Adj94607 Chimeric
6	533.5	85.6	120	7 ADJ94601	Adj94601 Mouse ant
7	529	84.9	123	6 AAO27201	Aao27201 Murine an
8	525.5	84.3	140	2 AAR55215	Aar55215 Murine va
9	525.5	84.3	412	4 AAB30694	Aab30694 A fusion
10	525.5	84.3	412	6 ABJ39009	Abj39009 B9E9 scFv
11	524.5	84.2	140	6 ABR55873	Abr55873 Anti-CD20
12	524.5	84.2	140	6 ABU08394	Abu08394 Murine an
13	524.5	84.2	140	7 ADC6270	Adc6270 Mouse ant
14	524.5	84.2	140	7 ADE85690	Ade85690 Murine im
15	524.5	84.2	140	7 ADE73084	Ade73084 Murine FU
16	524.5	84.2	140	7 ADF60661	Adf60661 Protein r
17	524.5	84.2	140	8 ADN49734	Adn49734 Mature va
18	524.5	84.2	140	8 ADU74410	Adu74410 Mouse ant
19	524.5	84.2	140	9 ADV92492	Adv92492 2B8 heavy
20	524.5	84.2	140	9 ADV98555	Adv98555 Novel chi
21	524.5	84.2	140	9 ADZ59909	Adz59909 Glycoprot
22	524.5	84.2	360	5 AAE27924	Aae27924 Human CH2
23	524.5	84.2	360	6 ABB82833	Abb82833 Antibody
24	524.5	84.2	368	9 ADW77074	Adw77074 Heavy cha

25	524.5	84.2	451	8 ADL92472	Adl92472 Antibody
26	524.5	84.2	451	8 ADL92473	Adl92473 Improved
27	524.5	84.2	451	8 ADU68155	Adu68155 Novel var
28	524.5	84.2	451	8 ADU68154	Adu68154 Novel var
29	524.5	84.2	470	3 AAB08026	Aab08026 A dimeric
30	524.5	84.2	470	5 AAE27923	Aae27923 Human C2B
31	524.5	84.2	470	6 ABB82832	Abb82832 Antibody
32	524.5	84.2	470	9 ADV92496	Adv92496 Anti-CD20
33	524.5	84.2	470	9 ADV98559	Adv98559 Novel chi
34	524.5	84.2	626	9 ADV92500	Adv92500 CD20VH/FC
35	524.5	84.2	626	9 ADV98563	Adv98563 Novel chi
36	524.5	84.2	641	9 ADV92502	Adv92502 CD20VH/FC
37	524.5	84.2	641	9 ADV98565	Adv98565 Novel chi
38	524.5	84.2	657	9 ADV92504	Adv92504 FL/FC/CD2
39	524.5	84.2	657	9 ADV98567	Adv98567 Novel chi
40	523	83.9	122	9 ADV21492	Adv21492 Human ant
41	523	83.9	122	9 ADZ83548	Adz83548 CD20 VH
42	523	83.9	490	9 ADV21539	Adv21539 Mature fo
43	523	83.9	491	9 ADZ83606	Adz83606 CD3 speci
44	523	83.9	491	9 ADZ83598	Adz83598 CD3 speci
45	523	83.9	491	9 ADZ83602	Adz83602 CD3 speci

ALIGNMENTS

RESULT 1  
ADO32093  
ID ADO32093 standard; protein; 118 AA.  
XX  
AC ADO32093;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Humanised mouse anti-CD33 antibody My9-6 heavy chain SEQ ID NO:9.  
XX

KW anti-CD33 antibody; epitope-binding fragment;  
KW complementarity-determining region; CDR; immunoconjugate; cytostatic;  
KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;  
KW My9-6; heavy chain.

XX Mus musculus.  
OS Homo sapiens.  
OS Synthetic.

XX WO2004043344-A2.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-US032737.

XX 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

XX Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

XX New antibodies that bind to CD33, useful for treating a disease  
XX associated with CD33 expression, such as myelodysplastic syndrome, acute  
XX or chronic myeloid leukaemia.

XX Claim 11; SEQ ID NO 9; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its  
XX epitope-binding fragment comprising: (a) at least one complementary-  
XX determining region (CDR); or (b) at least heavy chain variable region  
XX comprising 3 CDRs, and at least one light chain variable region, where  
XX the CDR has the ability to bind CD33. Also described: (1) an  
XX immunoconjugate comprising the antibody or its epitope-binding fragment  
XX linked to a drug or prodrug; (2) a composition comprising the antibody or

CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment,  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 heavy  
 CC chain variable region, which is used in an example from the present  
 CC invention.

XX SQ Sequence 118 AA;

Query Match 100.0%; Score 623; DB 8; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKTPQGQGLEWGVYIPGNDISY 60

Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKTPQGQGLEWGVYIPGNDISY 60

QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 118

Db 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 118

RESULT 2

ID ADO32091  
 AD032091 standard; protein; 118 AA.

AC ADO32091;

DT 12-AUG-2004 (first entry)

XX Mouse anti-CD33 antibody My9-6 heavy chain variable region SEQ ID NO:7.

DE anti-CD33 antibody; epitope-binding fragment;  
 KW complementarity-determining region; CDR; immunoconjugate; cytostatic;  
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;  
 KW heavy chain.

XX Mus musculus.

XX WO2004043344-A2.

XX 27-MAY-2004.

PP 05-NOV-2003; 2003WO-US032737.

PR 07-NOV-2002; 2002US-0424332P.

XX (IMMU-) IMMUNOGEN INC.

XX Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

DR N-PSDB; ADO32140.

XX New antibodies that bind to CD33, useful for treating a disease  
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute  
 PT or chronic myeloid leukemia.

XX Claim 5; SEQ ID NO 7; 124pp; English.

XX The present invention describes an isolated anti-CD33 antibody or its  
 CC epitope-binding fragment comprising: (a) at least one complementarity-  
 CC determining region (CDR); or (b) at least heavy chain variable region  
 CC comprising 3 CDRs, and at least one light chain variable region, where  
 CC the CDR has the ability to bind CD33. Also described: (1) an  
 CC immunoconjugate comprising the antibody or its epitope-binding fragment  
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or  
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment,  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents the mouse anti-CD33 antibody My9-6 heavy chain  
 CC variable region, which is used in an example from the present invention.

XX SQ Sequence 118 AA;

Query Match 98.4%; Score 613; DB 8; Length 118;  
 Best Local Similarity 98.3%; Pred. No. 9.3e-44;  
 Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKTPQGQGLEWGVYIPGNDISY 60

Db 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKTPQGQGLEWGVYIPGNDISY 60

QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 118

Db 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTVTS 118

RESULT 3

ADO32157

ID ADO32157 standard; protein; 117 AA.

XX ADO32157;

XX 12-AUG-2004 (first entry)

XX Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:73.

XX anti-CD33 antibody; epitope-binding fragment;

XX complementarity-determining region; CDR; immunoconjugate; cytostatic;

XX antibody; myelodysplastic syndrome; acute myeloid leukaemia;

XX chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.

XX Mus musculus.



```

PN WO2004043344-A2.
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US032737.
XX
PR 07-NOV-2002; 2002US-0424332P.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Hoffee MG, Tavares D, Lutz RJ;
XX
DR WPI; 2004-411619/38.
XX
PT New antibodies that bind to CD33, useful for treating a disease
PT associated with CD33 expression, such as myelodysplastic syndrome, acute
PT or chronic myeloid leukemia.
XX
PS Example 3; SEQ ID NO 73; 124pp; English.
XX
CC The present invention describes an isolated anti-CD33 antibody or its
CC epitope-binding fragment comprising: (a) at least one complementarity-
CC determining region (CDR); or (b) at least heavy chain variable region
CC comprising 3 CDRs, and at least one light chain variable region, where
CC the CDR has the ability to bind CD33. Also described: (1) an
CC immunoconjugate comprising the antibody or its epitope-binding fragment
CC linked to a drug or prodrug; (2) a composition comprising the antibody or
CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
CC composition comprising the immunoconjugate, composition or the antibody
CC defined above, or its epitope-binding fragment, and a pharmaceutical
CC agent; (4) a diagnostic reagent comprising the antibody defined above,
CC where the antibody or antibody fragment is labelled; (5) inhibiting the
CC growth of a cell expressing CD33 by contacting the cell with the above
CC defined antibody or its epitope-binding fragment; immunoconjugate, or
CC (pharmaceutical) composition; (6) determining whether a biological sample
CC contains a myelogenous cancer cell; (7) an improved antibody or its
CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
CC polynucleotide encoding the antibody or its epitope-binding fragment
CC defined above; (9) an isolated polynucleotide encoding a light or heavy
CC chain of the antibody defined above or its epitope-binding fragment; (10)
CC a recombinant vector comprising the polynucleotide; (11) a host cell
CC transformed with the recombinant vector; (12) producing an antibody or
CC its epitope-binding fragment having the ability to bind CD33; and (13)
CC obtaining CD33 from a biological material. The anti-CD33 antibody has
CC cytostatic activity. The antibody or its epitope-binding fragment,
CC immunoconjugate, composition can be used for treating a subject having a
CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
CC It can also be used for inhibiting the growth of cells expressing CD33,
CC and for in vivo imaging or as affinity purification agents. The present
CC sequence represents a mouse anti-CD33 antibody heavy chain homologous
CC amino acid sequence, which is used in an example from the present
XX invention.
XX
SQ Sequence 117 AA;
Query Match 97.8%; Score 609; DB 8; Length 117;
Best Local Similarity 98.3%; Pred. No. 2e-43;
Matches 115; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
QY 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTITVTS 117
DB 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTITVTS 117
QY 118 $ 118
DB 121 $ 121
RESULT 5
ADJ94607
ID ADJ94607 standard; protein; 121 AA.
XX
AC ADJ94605;
XX
DT 06-MAY-2004 (first entry)
XX
DE Chimeric anti-CD20 antibody variable heavy chain.
XX
KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;
KW IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
KW thrombocytopenia; lupus; rheumatoid arthritis;
KW heavy chain variable region.
XX
OS Chimeric.
OS Unidentified.
XX
PN WO2003068821-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-GB000665.
XX
PR 14-FEB-2002; 2002US-0356132P.
PR 07-OCT-2002; 2002US-0416232P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Hansen H, Qu Z, Goldenberg DM;
XX
DR WPI; 2003-697522/66.
DR N-PSDB; ADJ94604.
XX
PT New humanized anti-CD20 monoclonal antibody (MAb) that retains
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT of the murine anti-CD20 MAb, useful for treating B-cell lymphoma,
PT leukemia or an autoimmune diseases.
XX
PS Disclosure; Fig 2B; 106pp; English.
XX
CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
CC (MAb) or its antigen-binding fragment containing the complementarity
CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable
CC region and the framework regions (FRs) of at least one human IV1AB
CC variable region. The antibodies of the invention are useful for
CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
CC present amino acid sequence represents a chimeric anti-CD20 antibody
CC variable heavy chain.
XX
SQ Sequence 121 AA;
Query Match 86.4%; Score 538.5; DB 7; Length 121;
Best Local Similarity 84.3%; Pred. No. 1.7e-37;
Matches 102; Conservative 7; Mismatches 9; Indels 3; Gaps 1;
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTTPGQGLEWVGVIYFGNDISY 60
QY 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 117
DB 61 NQPKQKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 120
QY 118 $ 118
DB 121 $ 121
RESULT 5
ADJ94607
ID ADJ94607 standard; protein; 121 AA.
XX
AC ADJ94607;
XX

```

```

DT 06-MAY-2004 (first entry)
XX Chimeric anti-CD20 antibody variable heavy chain amino acid sequence.
DE
XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
KW IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
KW thrombocytopenia; lupus; rheumatoid arthritis;
KW heavy chain variable region.
XX
OS Chimeric.
OS Unidentified.
XX
PN WO2003068821-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-GB000665.
XX
PR 14-FEB-2002; 2002US-0356132P.
PR 07-OCT-2002; 2002US-0416232P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
PI Hansen H, Qu Z, Goldenberg DM;
XX
XX WPI; 2003-697522/66.
DR
XX New humanized anti-CD20 monoclonal antibody (MAB) that retains
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT of the murine anti-CD20 MAB, useful for treating B-cell lymphoma,
PT leukemia or an autoimmune diseases.
XX
XX Claim 22; Fig 4A; 106pp; English.
PS
XX The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
XX (MAB) or its antigen-binding fragment containing the complementarity
XX determining regions (CDRs) of at least one murine anti-CD20 Mab variable
XX region and the framework regions (FRs) of at least one human IV1AB
XX variable region. The antibodies of the invention are useful for
XX diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
XX disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
XX present amino acid sequence represents a chimeric anti-CD20 antibody
XX variable heavy chain.
XX
SQ Sequence 121 AA;
Query Match 86.4%; Score 538.5; DB 7; Length 121;
Best Local Similarity 84.3%; Pred. NO. 1.7e-37;
Matches 102; Conservative 7; Mismatches 9; Indels 3; Gaps 1;
QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
DB 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTVS 117
DB 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTVS 120
QY 118 S 118
DB 121 S 121
RESULT 6
ID ADJ94601 standard; protein; 120 AA.
XX
AC ADJ94601;
XX
DT 06-MAY-2004 (first entry)
XX
DE Mouse anti-CD20 antibody variable heavy chain.
XX
XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;
KW IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;
KW thrombocytopenia; lupus; rheumatoid arthritis;
KW heavy chain variable region; mouse; murine.
XX
OS Mus sp.
XX
PN WO2003068821-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-GB000665.
XX
PR 14-FEB-2002; 2002US-0356132P.
PR 07-OCT-2002; 2002US-0416232P.
XX
XX (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
PI Hansen H, Qu Z, Goldenberg DM;
XX
XX WPI; 2003-697522/66.
DR N-PSDB; ADJ94600.
XX
XX New humanized anti-CD20 monoclonal antibody (MAB) that retains
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting
PT of the murine anti-CD20 MAB, useful for treating B-cell lymphoma,
PT leukemia or an autoimmune diseases.
XX
XX Example 1; Fig 1B; 106pp; English.
PS
XX The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody
XX (MAB) or its antigen-binding fragment containing the complementarity
XX determining regions (CDRs) of at least one murine anti-CD20 Mab variable
XX region and the framework regions (FRs) of at least one human IV1AB
XX variable region. The antibodies of the invention are useful for
XX diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune
XX disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The
XX present amino acid sequence represents a mouse anti-CD20 antibody
XX variable heavy chain.
XX
SQ Sequence 120 AA;
Query Match 85.6%; Score 533.5; DB 7; Length 120;
Best Local Similarity 84.2%; Pred. NO. 4.3e-37;
Matches 101; Conservative 7; Mismatches 9; Indels 3; Gaps 1;
QY 2 VQLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 61
DB 1 VQLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60
QY 62 QKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTVS 118
DB 61 QKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTVS 120
RESULT 7
AAO27201
ID AAO27201 standard; protein; 123 AA.
XX
AC AAO27201;
XX
DT 17-SEP-2003 (first entry)
XX
DE Murine anti-CD20 antibody, 1F5, VH protein.
XX
XX Framework-patching; complementarity determining region; CDR; mouse;
KW murine; cytostatic activity; cancer; Non-Hodgkin's lymphoma;
KW gene therapy; rheumatoid arthritis; FR-patching; 1F5 VH; CD20; antibody.
XX
OS Mus sp.
XX

```

FH Key Location/Qualifiers  
 FT Domain 31..35  
 FT /note= "Complementarity determining region (CDR) 1"  
 FT Domain 50..66  
 FT /note= "Complementarity determining region (CDR) 2"  
 FT Domain 99..111  
 FT /note= "Complementarity determining region (CDR) 3"  
 XX WO2003002607-A1.  
 XX 09-JAN-2003.  
 XX 10-JUN-2002; 2002WO-US018512.  
 XX 27-JUN-2001; 2001US-00892613.  
 XX (LEUNG/) LEUNG S S.  
 XX Leung SS;  
 XX WPI; 2003-210245/20.  
 XX New re-engineered or framework-patched immunoglobulin, useful for  
 PT preparing a composition for treating cancer, preferably Non-Hodgkin's  
 PT lymphoma or rheumatoid arthritis.  
 XX Example 2; Fig 7a; 66pp; English.  
 XX The invention relates to a novel re-engineered or framework (FR)-patched  
 CC immunoglobulin, containing the heavy and/or light chain variable region  
 CC (VH/VL) sequences from a parent antibody. Within these chains, at least  
 CC one of the compartmentalised framework sequences, defined as FR1, FR2,  
 CC FR3 and FR4 are replaced, or patched, by the corresponding framework  
 CC sequences from the heavy and light chain immunoglobulin region of a  
 CC different species. The FR-patched immunoglobulin binds specifically to an  
 CC antigen with affinity comparable to, or within 3-fold of, that of the  
 CC parent immunoglobulin. The invention discloses the process of FR-patching  
 CC which is used to generate re-engineered immunoglobulin chains having one  
 CC or more complementarity determining regions (CDR's) from a donor  
 CC immunoglobulin and portions of framework sequences from one or more human  
 CC or primate immunoglobulins. The molecules obtained demonstrate cytostatic  
 CC activity as well as reduced or eliminated immunogenicity, whilst  
 CC maintaining the specificity and affinity of the parent antibody. The FR-  
 CC patched immunoglobulin is useful during the preparation of a composition  
 CC for treating cancer, preferably Non-Hodgkin's lymphoma and also during  
 CC the treatment of rheumatoid arthritis. Furthermore, the molecules of the  
 CC invention may also prove useful in gene therapy. The current sequence is  
 CC that of the murine anti-CD20 antibody, 1F5, VH protein of the invention  
 XX  
 SQ Sequence 123 AA;  
 Query Match 84.9%; Score 529; DB 6; Length 123;  
 Best Local Similarity 82.0%; Pred. No. 1.1e-36;  
 Matches 100; Conservative 9; Mismatches 9; Indels 4; Gaps 1;  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYFGNDISY 60  
 DB 1 QVQLRQFGLVLPFGASVKMSCKASGYTFTSYNMHWVKQTTPGQGLEWIGAIYFGNGDTSY 60  
 QY 61 NQKPFQKATLTADKSSSTAYMQLSSLTSEDSAVVYCAR----EVRLRYFDVWGQGTITVTV 116  
 DB 61 NQKPFQKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSHYGSNYVDYFDVWGQGTITLV 120  
 QY 117 SS 118  
 DB 121 SS 122  
 RESULT 8  
 AAR55215  
 ID AAR55215 standard; protein; 140 AA.  
 XX  
 AC AAR55215;

XX 25-MAR-2003 (revised)  
 DT 01-FEB-1995 (first entry)  
 XX  
 DB Murine variable region heavy chain from 2B8.  
 XX  
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;  
 KW cell lysis.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9411026-A2.  
 XX  
 PD 26-MAY-1994.  
 XX  
 PF 12-NOV-1993; 93WO-US010953.  
 XX  
 PR 13-NOV-1992; 92US-00978891.  
 PR 03-NOV-1993; 93US-00149099.  
 XX  
 XX (IDEC-) IDEC PHARM CORP.  
 XX  
 XX Anderson DR, Rastetter WH, Hanna N, Leonard JE, Newman RA;  
 PI Reff ME;  
 XX  
 DR WPI; 1994-183162/22.  
 DR N-PSDB; AAQ65631.  
 XX  
 XX Treating B cell lymphoma with chimeric antibody - against CD20, causing  
 PT rapid depletion of peripheral B cells, also new antibodies and  
 PT hybridomas.  
 XX  
 PS Disclosure; Fig 5; 101pp; English.  
 XX  
 CC The sequence is the murine variable region heavy chain derived from  
 CC murine anti-CD20 monoclonal antibody 2B8. See also AAQ65629-35. (Updated  
 CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct  
 CC PI field.)  
 XX  
 SQ Sequence 140 AA;  
 Query Match 84.3%; Score 525.5; DB 2; Length 140;  
 Best Local Similarity 81.8%; Pred. No. 2.4e-36;  
 Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;  
 QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYFGNDISY 60  
 DB 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKQTTPGQGLEWIGAIYFGNGDTSY 79  
 QY 61 NQKPFQKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRL---RYFDVWGQGTITVTVS 117  
 DB 80 NQKPFQKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTYYGDSYFNVWGAGTTVTVS 139  
 QY 118 S 118  
 DB 140 A 140  
 RESULT 9  
 AAB30694  
 ID AAB30694 standard; protein; 412 AA.  
 XX  
 AC AAB30694;  
 XX  
 XX 02-APR-2001 (first entry)  
 DT  
 DE A fusion of anti-CD20 single chain antibody/streptavidin.  
 XX  
 KW Streptavidin; tumour cell; cancer; adenocarcinoma;  
 KW hematological malignancy; B9E9.  
 XX  
 OS Synthetic.  
 OS Streptomyces avidinii.

```

OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT 1. .108
FT /note= "VL chain"
FT Peptide
FT 109. .126
FT /note= "linker"
FT Protein
FT 127. .248
FT /note= "VH chain"
FT Peptide
FT 249. .253
FT /note= "linker"
FT Protein
FT 254. .412
FT /note= "streptavidin"
XX
PN WO200075333-A1.
XX
PD 14-DEC-2000.
XX
XX 05-JUN-2000; 2000WO-US015595.
XX
XX 07-JUN-1999; 99US-0137900P.
XX 03-DEC-1999; 99US-0168976P.
XX
XX (NEOR-) NEORX CORP.
XX
XX Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX WPI; 2001-091213/10.
XX DR N-PSDB; AAC86563.
XX
XX New vector constructs for expressing genomic streptavidin fusion proteins
XX PT which are useful for targeting tumor cells associated with cancer, e.g.
XX PT adenocarcinomas.
XX
XX Example 2; Fig 11B; 100pp; English.
XX
XX The present sequence represents a fusion of an anti-CD20 single chain
XX antibody (B9E9) streptavidin. The fusion protein is expressed using
XX vectors of the invention. The specification describes vector constructs
XX for expressing streptavidin fusion proteins. The vector comprises a
XX nucleic acid encoding streptavidin or its functional variant operatively
XX linked to a promoter, and a cloning site for insertion of a second
XX nucleic acid sequence encoding a polypeptide to be fused with
XX streptavidin, interposed between the promoter and the first nucleic acid
XX sequence. Alternatively, the vector construct comprises a nucleic acid,
XX operatively linked to a promoter, encoding a polypeptide to be fused with
XX streptavidin, and a cloning site for insertion of a second nucleic acid
XX encoding at least 129 amino acids of streptavidin or its functional
XX variant. The fusion proteins are useful for targeting tumour cells,
XX particularly tumour cells associated with cancer, e.g. adenocarcinomas or
XX hematological malignancies. The vector construct is useful for expressing
XX of streptavidin fusion proteins. In particular, these are useful as tools
XX for medical diagnostics and therapeutic purposes, e.g. for detecting the
XX presence or absence of, or treating, a target site within a mammalian
XX host
XX
XX Sequence 412 AA;
SQ
Query Match 84.3%; Score 525.5; DB 4; Length 412;
Best Local Similarity 83.6%; Pred. No. 7e-36;
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;
QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKPTQGGLEWGVVYPGNDISY 60
DB 128 QVQLVQSGAEVVKPGASVKMSCKASGYTFTSYNMHWVKQTGQGLEWIGAIYPGNGDTSY 187
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSNAVYYCAREVRLR---YEDVWGQGTIVTV 116
DB 188 NQKFGKATLTADKSSSTAYMQLSLTSDSNAVYYCAR-AQLRPNWYFDVWGAGTIVTV 246
QY 117 SS 118
DB 247 SS 248

```

```

RESULT 10
ABJ39009
ID ABJ39009 standard; protein; 412 AA.
XX
XX AC ABJ39009;
XX
XX DT 09-OCT-2003 (first entry)
XX
XX DE B9E9 scFvSA fusion protein A amino acid sequence.
XX
XX KW Streptavidin fusion protein; SA; Streptomyces avidinii; biotin; scFvSA;
XX anti-CD25 antibody; antigen binding fragment; cytostatic; gene therapy;
XX cell-specific targeting agents; single chain; tumour; B989.
XX
XX OS Streptomyces avidinii.
XX Mus sp.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1. .106
XX FT /note= "VL region of the fusion protein"
XX FT Region
XX FT 107. .127
XX FT /note= "Synthetic linker region (pKOD)"
XX FT Region
XX FT 128. .247
XX FT /note= "VH region of the fusion protein"
XX FT Region
XX FT 248. .253
XX FT /note= "Synthetic linker region"
XX FT Region
XX FT 254. .412
XX FT /note= "Streptavidin region of the fusion protein"
XX
XX PN WO2003050260-A2.
XX
XX PD 19-JUN-2003.
XX
XX PF 06-DEC-2002; 2002WO-US039429.
XX
XX PR 07-DEC-2001; 2001US-00013173.
XX PR 17-MAY-2002; 2002US-00150762.
XX PR 16-SEP-2002; 2002US-00244821.
XX
XX PA (NEOR-) NEORX CORP.
XX
XX PI Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX PI Dearstyne EA;
XX
XX DR WPI; 2003-532908/50.
XX DR N-PSDB; ABT43498.
XX
XX PT New vector construct for expressing genomic streptavidin fusion proteins
XX useful as diagnostic markers or as cell-specific targeting agents.
XX
XX PS Disclosure; Fig 11B; 156pp; English.
XX
XX CC This invention relates to novel vector constructs for the expression of
XX streptavidin fusion proteins. Streptavidin (SA) is produced by
XX Streptomyces avidinii and specifically binds water-soluble biotin. The
XX vectors comprise a nucleic acid sequence encoding genomic streptavidin, a
XX promoter operatively linked to the nucleic acid sequence encoding an anti-
XX CD25 antibody or its antigen binding fragment. The fusion proteins
XX encoded are known as single chain antibody-genomic streptavidin fusion
XX proteins (scFvSA). The vectors may have cytostatic activity when used in
XX gene therapy. The vectors may be useful in expressing genomic
XX streptavidin fusion cassettes. The fusion proteins may be used as
XX diagnostic markers or as cell-specific targeting agents. These may also
XX be used in treating tumours. The present sequence is the amino acid
XX sequence of the B9E9 single chain antibody-genomic streptavidin fusion
XX protein of the invention
XX
XX Sequence 412 AA;
SQ

```

Query Match 84.3%; Score 525.5; DB 6; Length 412;  
 Best Local Similarity 83.6%; Pred. No. 7e-36;  
 Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWGVLYPGNDISY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 128 QVQLVQSGAEVVKPGASVKMSCKASGYTFTSYNHHWVKQTTPGQGLEWIGAIYPGNGDTSY 187  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR----YFDVWGQGTITVTV 116  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 188 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAR-AQLRPNYWFYFDVWGAGTITVTV 246  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 117 SS 118  
 ||  
 Db 247 SS 248

RESULT 11  
 ABR55873  
 ID ABR55873 standard; protein; 140 AA.  
 XX AC ABR55873;  
 XX DT 02-SEP-2003 (first entry)  
 XX DE Anti-CD20 antibody heavy chain variable region.  
 XX KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan; CD20;  
 XX KW antibody; mouse.  
 XX OS Mus musculus.  
 XX PN WO2003031464-A2.  
 XX PD 17-APR-2003.  
 XX PF 09-OCT-2002; 2002WO-US032263.  
 XX PR 10-OCT-2001; 2001US-0328523P.  
 XX PR 19-OCT-2001; 2001US-0344692P.  
 XX PR 28-NOV-2001; 2001US-0334233P.  
 XX PR 28-NOV-2001; 2001US-0334301P.  
 XX PR 07-JUN-2002; 2002US-0387292P.  
 XX PR 25-JUN-2002; 2002US-0391777P.  
 XX PR 17-JUL-2002; 2002US-0396594P.  
 XX PR 16-AUG-2002; 2002US-040249P.  
 XX PR 28-AUG-2002; 2002US-0407527P.  
 XX PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 XX PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;  
 XX DR WPI; 2003-449162/42.  
 XX DR N-PSDB; ACC78895.

Remodeling a peptide, by removing a saccharyl subunit from the peptide to form truncated glycan, and adding or deleting glycosyl groups to a peptide and/or adding modifying group of a peptide to remodel the peptide.

Example; Fig 83B; 900pp; English.

The invention relates to a cell-free, in vitro method of remodeling a peptide. The method involves removing a saccharyl subunit from the peptide, thus forming a truncated glycan, and contacting the truncated glycan with at least one glycosyltransferase and at least one glycosyl donor under conditions suitable to transfer at least one glycosyl donor to the truncated glycan, thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-CSF) peptide, interferon alpha peptide, interferon beta peptide, Factor VIIa peptide, Factor IX peptide, follicle stimulating hormone peptide, erythropoietin (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF) peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-P)

CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA) peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti-HER2 antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide, insulin peptide, hepatitis B surface antigen (HbsAg), human growth hormone (HGH) peptide, and a modifying group, where the modifying group is covalently attached to the peptide through an intact glycosyl linking group. The method is useful for a cell-free, in vitro method of remodeling the above mentioned peptides. The present sequence represents the murine anti-CD20 antibody heavy chain mature variable region

XX SQ Sequence 140 AA;

Query Match 84.2%; Score 524.5; DB 6; Length 140;  
 Best Local Similarity 81.8%; Pred. No. 2.9e-36;  
 Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWGVLYPGNDISY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNHHWVKQTTPGQGLEWIGAIYPGNGDTSY 79  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCAREVRLR---YFDVWGQGTITVTVS 117  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGDMYFNVWGAGTITVTVS 139  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 118 S 118  
 ;  
 Db 140 A 140

RESULT 12  
 ABU08394  
 ID ABU08394 standard; protein; 140 AA.  
 XX AC ABU08394;  
 XX DT 11-JUN-2003 (first entry)  
 XX DE Murine anti-CD20 antibody heavy chain variable region.  
 XX DE B cell lymphoma; chimeric anti-CD20 antibody; cytostatic; mouse; VH;  
 XX KW expression vector; murine; heavy chain; variable region.  
 XX OS Mus sp.

XX FH Key Location/Qualifiers  
 XX FT Peptide 1..19 /label= Signal\_peptide  
 XX FT Protein 20..140 /label= Mature\_anti-CD20\_antibody\_VH\_region  
 XX FN US2002197255-A1.  
 XX XX  
 XX PD 26-DEC-2002.  
 XX PF 25-JUL-2001; 2001US-00911703.  
 XX PR 07-JUN-1995; 95US-00475813.  
 XX XX  
 XX PA (IDEC-) IDEC PHARM CORP.

XX PI Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;  
 XX PI Rastetter WH;

XX DR WPI; 2003-352746/33.  
 XX DR N-PSDB; ABX94209.

XX XX  
 XX PT Treating B cell lymphoma in humans, comprises administering  
 XX PT immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled  
 XX PT anti-CD20 antibodies to the human.

PS Example; Fig 5; Sipp; English.

XX The present invention relates to a method for treating B cell lymphoma.

CC The method comprises administering at a first administration period, an

CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or

CC administering, at a second administration period, a radiolabelled anti-

CC CD20 antibody, to the human subject. The invention also discloses

CC expression vectors that may be used in the method of the present

CC invention. The method is useful for treating B cell lymphoma in humans.

CC The present sequence represents murine anti-CD20 antibody heavy chain

CC variable region

XX Sequence 140 AA;

SQ

Query Match 84.2%; Score 524.5; DB 6; Length 140;

Best Local Similarity 81.8%; Pred. No. 2.9e-36;

Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDLSY 60

DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDLSY 79

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 117

DB 80 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 139

QY 118 S 118

DB 140 A 140

RESULT 14

AD85690

ID ADE85690 standard; protein; 140 AA.

XX

AC ADE85690;

XX

DT 29-JAN-2004 (first entry)

XX

DE Murine immunoglobulin heavy chain variable region.

XX

KW B cell lymphoma; anti-CD20; peripheral B cell; C2B8;

KW immunoglobulin heavy chain variable region; mouse; antibody.

XX

OS Mus sp.

XX

PN US2003147885-A1.

XX

PD 07-AUG-2003.

XX

PF 11-SEP-2002; 2002US-00238681.

XX

PR 13-NOV-1992; 92US-00978891.

PR 03-NOV-1993; 93US-00149099.

PR 29-AUG-1997; 97US-00921060.

XX

PA (IDEC-) IDEC PHARM CORP.

XX

PI Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;

PI Rastetter WH;

XX

DR WPI: 2003-897520/82.

DR N-PSDB; ADE85689.

XX

PT Treating B cell lymphoma by administering an anti-CD20 antibody and at

PT least one chemotherapeutic agent.

XX

PS Example; SEQ ID NO 11; 52pp; English.

XX

CC The invention relates to an improved method for treating B cell lymphoma

CC comprising administering an anti-CD20 antibody. The improvement comprises

CC administering at least one chemotherapeutic agent. The antibody causes a

CC substantial depletion of peripheral B cells. The antibody is chimeric

CC anti-CD20 or C2B8. The method is useful for treating B cell lymphoma.

CC This sequence represents a murine immunoglobulin heavy chain variable

CC region used in the method of the invention.

XX

SQ Sequence 140 AA;

Query Match 84.2%; Score 524.5; DB 7; Length 140;

PS Example; Fig 5; Sipp; English.

XX The present invention relates to a method for treating B cell lymphoma.

CC The method comprises administering at a first administration period, an

CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or

CC administering, at a second administration period, a radiolabelled anti-

CC CD20 antibody, to the human subject. The invention also discloses

CC expression vectors that may be used in the method of the present

CC invention. The method is useful for treating B cell lymphoma in humans.

CC The present sequence represents murine anti-CD20 antibody heavy chain

CC variable region

XX Sequence 140 AA;

SQ

Query Match 84.2%; Score 524.5; DB 6; Length 140;

Best Local Similarity 81.8%; Pred. No. 2.9e-36;

Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDLSY 60

DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDLSY 79

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 117

DB 80 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREVRLR---YFDVMGQGTTVTVS 139

QY 118 S 118

DB 140 A 140

RESULT 13

ADC66270

ID ADC66270 standard; protein; 140 AA.

XX

AC ADC66270;

XX

DT 18-DEC-2003 (first entry)

XX

DE Mouse anti-CD20 antibody heavy chain variable region.

XX

KW immunosuppressant; cytostatic; antibody; CD20;

KW N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine;

KW sugar chain; cancer; immune disorder.

XX

OS Mus musculus.

XX

PN WO2003055993-A1.

XX

PD 10-JUL-2003.

XX

PF 25-DEC-2002; 2002WO-JP013534.

XX

PR 25-DEC-2001; 2001JP-00392753.

PR 09-APR-2002; 2002JP-00106948.

PR 01-NOV-2002; 2002JP-00319975.

XX

PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX

PI Shitara K, Sakurada M, Uchida K, Shinkawa T, Satoh M, Nakano R;

PI WPI: 2003-559274/52.

DR N-PSDB; ADC66269.

XX

PT Antibody binding to CD20 and having Fc-bound sugar chains of low fucose

PT content for treatment of cancer and immune disorders.

XX

PS Disclosure; SEQ ID NO 14; 200pp; Japanese.

XX

CC The invention relates to cells producing an antibody molecule

CC specifically binding to CD20 are new, in which the antibody contains N-

CC glycoside bond complex sugar chains bonded to the Fc region of the

CC antibody peptide chains, of which less than 20% have a fucose residue



**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:25:51 ; Search time 17.8788 Seconds  
(without alignments)  
635.031 Million cell updates/sec

Title: US-10-700-632-9  
Perfect score: 623  
Sequence: 1 QVQLQQPGAEVVKPGASVKM.....EVLRLYFDVWGQTTVTWSS 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	496	79.6	120	2 B22769	Ig heavy chain V r
2	486.5	78.1	119	2 PL0089	Ig heavy chain V r
3	486	78.0	118	2 S38717	Ig heavy chain V r
4	483.5	77.6	138	2 E32513	Ig heavy chain pre
5	482.5	77.4	120	2 S25175	Ig heavy chain V r
6	482.5	77.4	136	2 PL0208	Ig heavy chain pre
7	479.5	77.0	138	2 S21810	Ig heavy chain V r
8	478	76.7	120	2 G28195	Ig heavy chain V r
9	477	76.6	115	2 A54378	Ig heavy chain V r
10	472	75.8	101	2 S42184	Ig gamma chain V r
11	472	75.8	101	2 S42179	Ig gamma chain V r
12	472	75.8	102	2 S42180	Ig gamma chain V r
13	471	75.6	131	2 S66537	Ig heavy chain V r
14	470.5	75.5	117	1 MHMSJ5	Ig heavy chain V r
15	470.5	75.5	133	2 S20846	Ig heavy chain V r
16	470	75.4	139	1 MHMS18	Ig heavy chain pre
17	470	75.4	287	4 PC4402	pe1B leader/Ig hea
18	468	75.1	116	2 S53751	antibody Fab Jel 1
19	468	75.1	120	2 F28195	Ig heavy chain V r
20	468	75.1	135	2 A30577	Ig heavy chain pre
21	467	75.0	133	2 PC1155	Ig heavy chain pre
22	467	75.0	137	1 G2MS43	Ig heavy chain pre
23	466.5	74.9	246	2 S38950	Ig gamma chain - m
24	466.5	74.9	446	2 S40295	Ig gamma-2a chain
25	466	74.8	120	2 S41394	Ig heavy chain V r
26	466	74.8	141	2 A39276	Ig heavy chain pre
27	464.5	74.6	117	1 MHMS4E	Ig heavy chain V r
28	464.5	74.6	140	2 T01407	Ig heavy chain (my
29	462	74.2	115	2 C27563	Ig heavy chain V r

ALIGNMENTS

RESULT 1

B22769  
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 16-Aug-1996  
C:Accession: B22769  
R:Dildrop, R.; Brugemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.  
EMEO J. 1, 635-640, 1982  
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between  
A:Reference number: A90971; MUID:84236026; PMID:7188353  
A:Accession: B22769  
A:Molecule type: protein  
A:Residues: 1-120 <DIL>  
A:Cross-references: UNIPARC:UPI0000176B76  
A:Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2  
A:Note: peptides and unsequenced residues were positioned by homology with the B1-8 seq  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 496; DB 2; Length 120;  
Best Local Similarity 77.5%; Pred. No. 2.5e-37;  
Matches 93; Conservative 12; Mismatches 13; Indels 2; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKASGYFTFTSYIHNIKOTPGQLEWGVVPGNDISY 60  
Db 1 QVQLQQPGAEVVKPGASVKASGYFTFTSYMHVVKRQPGGLEWIGRIHPSDSTNY 60  
Qy 61 NQKFOGKATLTADKSTTAYMOLSLTSDTSNAVYCAR--EVLRLYFDVWGQTTVTWSS 118  
Db 61 NQKFGKATLTVDKPSSTAYMOLSLTSDTSNAVYCARVDYVYSSFDYWGQTTLTWSS 120

RESULT 2

PL0089  
Ig heavy chain V region (12S18-1) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Mar-2000  
R:Meek, K.; Hasegawa, C.; Pollok, B.; Alkan, S.S.; Braib, M.; Slaoui, M.; Urbain, J.;  
J. Exp. Med. 169, 519-533, 1989  
A:Title: Structural characterization of antiidiotypic antibodies; evidence that Abs2a ar  
A:Reference number: PL0080; MUID:89094248; PMID:2492056  
A:Accession: PL0089  
A:Molecule type: mRNA  
A:Residues: 1-119 <ME>  
A:Cross-references: UNIPARC:UPI0000115F1B; GB:X58580; GB:Y00794; NID:g51591; PIDN:CAA414  
A:Note: the sequences shown here is from the VH region of an antiidiotypic monoclonal ant  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

```
Query Match      78.1%; Score 486.5; DB 2; Length 119;
Best Local Similarity 77.3%; Pred. No. 1.8e-36;
Matches 92; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPQGQLEWGVYIPGNDISY 60
Db 1 QVQLQEPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPQGQLEWGVYIPGSDYTN 60

Qy 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYICAR-EVRLRYFDVWGQTTVTSS 118
Db 61 NEKFKSKATLTADKSSSTAYMQLSLTSDSAVYICARNEGVAWYFDVWGQTTVAXSS 119

RESULT 3
S38717
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38717
R:Cimanis, A. Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38717
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <CIM>
A:Cross-references: UNIPARC:UPI0000117541; EMBL:X76020; NID:g416099; PIDN:CAA53607.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match      78.0%; Score 486; DB 2; Length 118;
Best Local Similarity 77.1%; Pred. No. 1.9e-36;
Matches 91; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPQGQLEWGVYIPGNDISY 60
Db 1 QDQLQQSGDLVKPGASVKMSCKASGYTFTSYTHWIKQTPQGQLEWIGYIHPYNDGSKY 60

Qy 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLRYFDVWGQTTVTSS 118
Db 61 NDKFKGKATLTADKSSSTAYMQLSLTSDSAVYICARENGFNFYFDVWGQTTVTSS 118

RESULT 4
E32513
Ig heavy chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C:Accession: E32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1998
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: E32513
A:Molecule type: DNA
A:Residues: 1-138 <KOF>
A:Cross-references: UNIPARC:UPI0000114D9D; GB:M20835; NID:g196945; PIDN:AAA38847.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:34-117/Domain: immunoglobulin homology <IMM>

Query Match      77.6%; Score 483.5; DB 2; Length 138;
Best Local Similarity 75.8%; Pred. No. 3.8e-36;
Matches 91; Conservative 15; Mismatches 11; Indels 3; Gaps 2;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPQGQLEWGVYIPGNDISY 60
Db 20 QVQLQQPGAEVVKPGASVKLSCKASGYTFTSYTHWIKQTPQGQLEWIGNIPGSSSTNY 79

Qy 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLRYF-DVWGQTTVTSS 118
```

```
Db 80 NEKFKSKATLTADKSSSTAYMQLSLTSDSAVYICARRL-YRYAMDYWGQTSVTSS 138

RESULT 5
S25175
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25175
R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histone
A:Reference number: S25174
A:Accession: S25175
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MON>
A:Cross-references: UNIPARC:UPI00001160C2; EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match      77.4%; Score 482.5; DB 2; Length 120;
Best Local Similarity 75.8%; Pred. No. 4e-36;
Matches 91; Conservative 11; Mismatches 15; Indels 3; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPQGQLEWGVYIPGNDISY 60
Db 1 QVQLQQPGAEVVKPGASVKLSCKASGYTFTSYTHWIKQTPQGQLEWIGNIDPSDSETHY 60

Qy 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYICAREV---RLRYFDVWGQTTVTSS 117
Db 61 NQKFKKATLTADKSSSTAYMQLSLTSDSAVYICAREKITDDYNYFDVWGQTTLTVS 120

RESULT 6
PL0208
Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/c)
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C:Accession: PL0208
R:Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reaction
A:Reference number: PL0207; MUID:90309764; PMID:1973259
A:Accession: PL0208
A:Molecule type: mRNA
A:Residues: 1-136 <SOU>
A:Cross-references: UNIPARC:UPI0000176C6F
A:Experimental source: hybridoma cell E225
C:Superfamily: immunoglobulin V region; immunoglobulin homology
P:1-19/Domain: signal sequence #status predicted <SIG>
P:34-117/Domain: immunoglobulin homology <IMM>
P:50-54/Region: complementarity-determining 1
P:59-85/Region: complementarity-determining 2
P:118-125/Region: complementarity-determining 3
P:118-121/Region: D region
P:122-136/Region: JH region

Query Match      77.4%; Score 482.5; DB 2; Length 136;
Best Local Similarity 74.6%; Pred. No. 4.6e-36;
Matches 88; Conservative 17; Mismatches 12; Indels 1; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYTHWIKQTPQGQLEWGVYIPGNDISY 60
Db 20 QVQLQQPGSELVRFPGASVKLSCKASGYTFTSYTHWIKQTPQGQLEWIGNIPGSGDSNY 79

Qy 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYICAREVRLRYFDVWGQTTVTSS 118
Db 80 DEKFKSKATLTADKSSSTAYMQLSLTSDSAVYICARGLAF-YFDHWGQTTLTVS 136

RESULT 7
```

A;Reference number: A54378; MUID:94165109; PMID:7509814

A;Accession: S42178

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <AGA>

A;Cross-references: UNIPARC:UPI0000176E3F; GB:S68981; NID:Q545744; PIDN:AAB3009S.1.; PDI:

A;Experimental source: spleen and myeloma cell line MOPC 315.43

A>Note: sequence inconsistent with nucleotide translation

C;Note: sequence extracted from NCBI backbone (NCBIN:144172, NCBIF:144173)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMV>

Query Match            76.6%; Score 477; DB 2; Length 115;  
Best Local Similarity   75.7%; Pred. No. 1.2e-35;  
Matches     87; Conservative   13; Mismatches   15; Indels       0; Gaps      0;

QY    1 QVOLQPGEAVKPGASVKMSCKASKGYTFTSYIHWIKQTPOGGLWGVVIYPGNDDISY 60  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db    1 EVLQQSGPELVKPGASVRISKASKGYTFYYIIHMKRPPQGQLGWIGWIYPNGNTKY 60  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY    61 NORFOGKATLTADKSSTAYMQLSLTSDESAVVYCAREVLRLRYFDVGOGTTVT 115  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db    61 NEKFEGKATLTADKSSTAYMQLSLTSDESAVFCASSGGYGWGQGTILT 115  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 10

S42184

Ig gamma chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change 06-Jun-1997  
C;Accession: S42184  
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993

A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spe-

A;Reference number: S42176; MUID:94009207; PMID:7691608

A;Accession: S42184

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <MOJ>

A;Cross-references: UNIPARC:UPI0000176ES9; EMBL:D25457

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: Immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMV>

Query Match            75.8%; Score 472; DB 2; Length 101;  
Best Local Similarity   89.7%; Pred. No. 2.9e-35;  
Matches     87; Conservative    6; Mismatches    4; Indels       0; Gaps      0;

QY    2 VOLQPGEAEVVPKGASVKMSCKASKGYTFTSYIHWIKQTPOGGLWGVVIYPGNDDISYN 61  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db    2 VLQLPQGAELVPKGASVKMSCKASKGYTFTSYNMHVWKQTPOGLEIWAIYPCGNDITSYN 61  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY    62 QKPFGKATLTADKSSTAYMQLSLTSDESAVVCAR 98  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db    62 QKEPKGATLTADKSSTAYMQLSLTSDESAVVCAR 98  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 11

S42179

Ig gamma chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1994 #sequence\_revision 21-Jul-1995 #text\_change 23-Jul-1999  
C;Accession: S42179  
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993

A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spe-

A;Reference number: S42176; MUID:94009207; PMID:7691608

A;Accession: S42179

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <MOJ>

A;Cross-references: UNIPARC:UPI00001165SF; EMBL:D25447; NID:9407816; PIDN:CAA80934.1.; PDI:



[illegible]

Search completed: May 9, 2006, 01:33:50  
Job time : 17.8788 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:41 ; Search time 108.039 Seconds  
(without alignments)  
770.577 Million cell updates/sec

Title: US-10-700-632-9  
Perfect score: 623  
Sequence: 1 QVQLQPQGAEVKPGASVKM.....EVRLRYFDVWGQTTVTYSS 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_05-80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	79.5	143	2	Q924Q0_MOUSE
2	490	78.7	143	2	Q91V67_MOUSE
3	488.5	78.4	120	2	Q5F211_MOUSE
4	484	77.7	143	2	Q924Q5_MOUSE
5	478.5	76.8	458	2	Q5BJ22_RAT
6	477.5	76.6	146	2	Q924R8_MOUSE
7	477	76.6	118	2	Q921C4_MOUSE
8	475	76.2	613	2	Q8VCX7_MOUSE
9	474	76.1	143	2	Q924R7_MOUSE
10	471	75.6	145	2	Q924R3_MOUSE
11	471	75.6	465	2	Q6PJ82_MOUSE
12	470.5	75.5	117	1	HV13_MOUSE
13	470.5	75.5	142	2	Q924Q1_MOUSE
14	470.5	75.5	470	2	Q7TWK1_MOUSE
15	470	75.4	139	1	HV07_MOUSE
16	470	75.4	145	2	Q924Q6_MOUSE
17	470	75.4	145	2	Q924Q7_MOUSE
18	470	75.4	145	2	Q924Q9_MOUSE
19	469	75.3	143	2	Q91VA2_MOUSE
20	467	75.0	137	1	HV11_MOUSE
21	466	74.8	482	2	Q8K172_MOUSE
22	465.5	74.7	134	2	Q65ZR6_MOUSE
23	465.5	74.7	144	2	Q924P5_MOUSE
24	465.5	74.7	468	2	Q569W9_MOUSE
25	464.5	74.6	117	1	HV12_MOUSE
26	464	74.5	137	2	Q924R6_MOUSE
27	463.5	74.4	117	2	Q9QXF0_MOUSE
28	462.5	74.2	140	2	Q924P8_MOUSE
29	462	74.2	109	2	Q9JL75_MOUSE
30	462	74.2	141	2	Q924Q4_MOUSE
31	462	74.2	143	2	Q924P6_MOUSE

32	461	74.0	143	2	Q924R0_MOUSE
33	460.5	73.9	483	2	Q4VAB6_MOUSE
34	460	73.8	145	2	Q924R1_MOUSE
35	459	73.7	590	2	Q4V9V8_MOUSE
36	458.5	73.6	140	2	Q924R2_MOUSE
37	458.5	73.6	146	2	Q924Q3_MOUSE
38	458.5	73.6	473	2	Q9D8L4_MOUSE
39	458.5	73.6	481	2	Q91WT1_MOUSE
40	457.5	73.4	120	1	HV03_MOUSE
41	457	73.4	145	2	Q924P7_MOUSE
42	457	73.4	145	2	Q924R4_MOUSE
43	456.5	73.3	117	2	Q9QXE9_MOUSE
44	456.5	73.3	142	2	Q924Q2_MOUSE
45	456	73.2	487	2	Q65ZL2_MOUSE

ALIGNMENTS

RESULT 1  
Q924Q0\_MOUSE  
ID Q924Q0\_MOUSE PRELIMINARY; PRT; 143 AA.  
AC Q924Q0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE V165-D-J-C mu protein (Fragment).  
GN Name=V165-D-J-C mu;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB069915; BAB63931.1; -; mRNA.  
DR PIR; PH1159; PH1159.  
DR HSSP; P01751; 1A6W.  
DR SMK; Q924Q0; 1-134.  
DR Ensembl; ENSMUSG00000021155; Mus musculus.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 143  
SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

Query Match 79.5%; Score 495; DB 2; Length 143;  
Best Local Similarity 78.0%; Pred. No. 4.9e-45;  
Matches 92; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
QY 1 QVQLQPQGAEVKPGASVKMSCKASGYTFTSYIHNIKPTPGQGLEWGVYPGNDISY 60  
Db 1 QVQLQPGALVKPGASVKMSCKASGYTFTSYITWVKRPGQGLEWIGDIYPGSGSTNY 60  
QY 61 NQKFGQKATLTADKSTTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQTTVTYSS 118  
Db 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYCAPDSNHLRYFDVWGQTTLTVTSS 118

RESULT 2  
Q91V67\_MOUSE  
ID Q91V67\_MOUSE PRELIMINARY; PRT; 143 AA.  
AC Q91V67;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).  
GN Name=VH186.2-D-J-C mu; Synonym=V304-D-J-C mu;





	Query Match	76.8%	Score 478.5	DB 2	Length 458
	Best Local Similarity	76.9%	Pred. No. 1.2e-42		
	Matches 93	Conservative 9	Mismatches 12	Indels 7	Gaps 2
Qy	1	QVQLQPGAEVWVPGASVKMSCKASGYTFTSYIIHWIKQTPTQGLGWVGVIYPGNDDISY	60		
Db	20	QVQLQSGAEIIVPGSSVKISCKASGYTFNTYDIHWIKQPGNGLEIHWIYPGNGNTKY	79		
Qy	61	NQPFQKATITADKSSITYAYMQLSSLTSEDSAVYYCAREVLRYP----	117		
Db	80	NQPFNGKATITADKSSITYAYMQLSSLTSEDSAVYFCARD----	135		

Db 136 S 136

RESULT 6

Q924R8\_MOUSE

ID Q924R8\_MOUSE PRELIMINARY; PRT; 146 AA.

AC Q924R8;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE VH186\_2-D-J-C mu protein (Fragment).

GN Name=VH186.2-D-J-C.mu;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

[2]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=3135311;

RA Corbet S., Hixn M., Roth C., Theze J., Fougereau M., Schiff C.;

RT "Allogeneic manipulation of the GAR idiotypic cascade. Immunization of C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-specific V genes as the original antigen.";

RT J. Immunol 141:779-784(1988).

DR EMBL, AB067781; BAB63266.1; -; mRNA.

DR PIR, F28833; F28833.

DR PIR, PH1105; PH1105.

DR PIR, PH1108; PH1108.

DR PIR, PH1114; PH1114.

DR PIR, PH1118; PH1118.

DR PIR, PH1119; PH1119.

DR PIR, PH1125; PH1125.

DR PIR, PH1126; PH1126.

DR PIR, PH1128; PH1128.

DR PIR, PH1129; PH1129.

DR PIR, PH1131; PH1131.

DR PIR, PH1134; PH1134.

DR PIR, PH1137; PH1137.

DR PIR, PH1139; PH1139.

DR PIR, PH1142; PH1142.

DR PIR, PH1144; PH1144.

DR PIR, PH1147; PH1147.

DR PIR, PH1149; PH1149.

DR PIR, PH1150; PH1150.

DR PIR, PH1151; PH1151.

DR PIR, PH1152; PH1152.

DR PIR, PH1153; PH1153.

DR HSSP, P01751; 1A6W.

DR SMR, Q924R8; 1-137.

DR Ensemble; ENSMUSG00000021155; Mus musculus.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig v.

DR SMART; SM00406; IGV; 1.

```
DR PROSITE; PS50835; IG_LIKE; 1.
ET NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460FLDFLB7538 CRC64;

Query Match
Best Local Similarity 76.6%; Score 477.5; DB 2; Length 146;
Matches 90; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQLEWVGVIYPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQLEWVGVIYPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREV---RLRYFDVWGQGTFTVVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NEKFSKATLTVDKPSSTAYMQLSLTSDSAVYVCARSYGSLSYFDYWGQGTFTVVS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 S 118
   |
Db 121 S 121

RESULT 7
ID Q921C4_MOUSE PRELIMINARY; PRT; 118 AA.
AC Q921C4
DC Q921C4
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Mattis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Mol. Immunol. 34:441-452(1997).
DR EMBL; U78801; AAD00293.1; -; mRNA.
DR SMR; Q921C4; 1-118.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR HSSP; P01751; INQB.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 908ECS59D31EC4FC CRC64;

Query Match
Best Local Similarity 76.6%; Score 477; DB 2; Length 118;
Matches 88; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQLEWVGVIYPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKTPQGQLEWVGVIYPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTFTVVS 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TQKFRGKATLTADKSSSTAYMQLSLTSDSAVYVCARRTVGGYFDYWGQGTFTVVS 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q8VCX7_MOUSE
ID Q8VCX7_MOUSE PRELIMINARY; PRT; 613 AA.
```

```
AC Q8VCX7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2464031;
RA Sikder S.K., Borden P., Gruezo F., Akolkar P.N., Bhattacharya S.B.,
RA Morrison S.L., Kabat E.A.;
RT "Amino acid substitutions in VH CDR2 change the idiotype but not the
RT antigen-binding of monoclonal antibodies to alpha(1----6)dextran."
RL J. Immunol. 142:888-893(1989).
DR EMBL; BC018315; AAH18315.1; -; mRNA.
DR PIR; C30562; C30562.
DR HSSP; P01751; IAGW.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR MGI; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0000187; P:activation of MAPK activity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . ; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 4.
```

```

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match
Best Local Similarity 76.2%; Score 475; DB 2; Length 613;
Matches 88; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVVKPGASVKLSCKASGYTFTSYIHWIKQTPGGGLEWVGVIYFGNDISY 60
Db 20 QVLOQPGAEVVKPGASVKLSCKASGYTFTSYIHWIKQTPGGGLEWVGVIYFGNDISY 118
QY 61 NQKFOGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFDVWGOGTTVTWSS 118
Db 80 NERFKGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFDVWGOGTTVTWSS 137

RESULT 9
Q924R7 MOUSE
ID Q924R7_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924R7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Names:VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAR idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
[3]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=3211160;
RA Kaartinen M., Rocca-Serra J., Makela O.;
RT "Combinatorial association of V genes: one VH gene codes for three
RT non-cross-reactive monoclonal antibodies each specific for a different
RT antigen (phoxazolone, NP or gat).";
RL Mol. Immunol. 25:859-865(1988).
DR EMBL; AB067787; BAB63272.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; JLO078; JLO078.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR PIR; S26744; S26744.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R3; 1-136.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 15648 MW; 51894D22EA9FDD47 CRC64;

Query Match
Best Local Similarity 76.1%; Score 474; DB 2; Length 143;
Matches 88; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVVKPGASVKLSCKASGYTFTSYIHWIKQTPGGGLEWVGVIYFGNDISY 60
Db 20 QVLOQPGAEVVKPGASVKLSCKASGYTFTSYIHWIKQTPGGGLEWVGVIYFGNDISY 118
QY 61 NQKFOGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFDVWGOGTTVTWSS 118
Db 80 NERFKGKATLTADKSSITAYMQLSSLTSEDSAVVYCAREVLRLYFDVWGOGTTVTWSS 137

RESULT 10
Q924R3 MOUSE
ID Q924R3_MOUSE PRELIMINARY; PRT; 145 AA.
AC Q924R3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Names:VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAR idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
[3]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=3211160;
RA Kaartinen M., Rocca-Serra J., Makela O.;
RT "Combinatorial association of V genes: one VH gene codes for three
RT non-cross-reactive monoclonal antibodies each specific for a different
RT antigen (phoxazolone, NP or gat).";
RL Mol. Immunol. 25:859-865(1988).
DR EMBL; AB067787; BAB63272.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; JLO078; JLO078.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR PIR; S26744; S26744.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R3; 1-136.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 15648 MW; 51894D22EA9FDD47 CRC64;

```

```
FT NON TER 1 1
FT NON TER 145 145
SQ SEQUENCE 145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;

Query Match 75.6%; Score 471; DB 2; Length 145;
Best Local Similarity 75.0%; Pred. No. 1.9e-42;
Matches 90; Conservative 12; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFSTYYIHWIKQTQPGGLEWGVYVPGNDLISY 60
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFSTYYIHWIKQTQPGGLEWGVYVPGNDLISY 60
QY 61 NOKFGKATLTADKSTTAYMQLSLTSDSAYVYCAREV--RLRYFDVWGQGTITVTVSS 118
DB 61 NEKFKSKATLTVDKSSSTAYMQLSLTSDSAYVYCAREGLYDGNWYFDVWGQGTITVTVSS 120

RESULT 11
Q6PJB2 MOUSE
ID Q6PJB2_MOUSE PRELIMINARY; PRT; 465 AA.
AC Q6PJB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN Name-Igh-1a;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins E.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Klausner R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; RAH18280.1; -; mRNA.
DR HSSP; P01865; 1KB5.
DR SMR; Q6PJB2; 20-461.
DR MGI; MGI:95443; Igh-1a.
DR GO; GO:0003823; Fractigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
```

```
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;

Query Match 75.6%; Score 471; DB 2; Length 465;
Best Local Similarity 75.4%; Pred. No. 7.6e-42;
Matches 89; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFSTYYIHWIKQTQPGGLEWGVYVPGNDLISY 60
DB 20 QVQLQSGAEVVKPGASVKLSCKASGYTFSTYYIHWIKQRPQGLGWIGYVSPYNDTKC 79
QY 61 NOKFGKATLTADKSTTAYMQLSLTSDSAYVYCAREVRLRYFDVWGQGTITVTVSS 118
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSDSAYVYCARGYV--FDYWGQGTITVTVSS 135

RESULT 12
HV13 MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG heavy chain V region J558.
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP PROTEIN SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
CC bind dextran differ from that shown at 1-7 positions, many of
CC which occur in the D and J segments.
CC -!- MISCELLANEOUS: This protein binds dextran.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A26242; MHMSJ5.
CC HSSP; P01751; INQB.
CC SMR; P01757; 1-117.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT DISULFID 22 96 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;

Query Match 75.5%; Score 470.5; DB 1; Length 117;
Best Local Similarity 76.3%; Pred. No. 1.7e-42;
Matches 90; Conservative 11; Mismatches 16; Indels 1; Gaps 1;
```

Qy 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYFGNDISY 60  
 Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYFGNDISY 60  
 Qy 61 NQKFOGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTIVTVSS 118  
 Db 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYVCARD-RYWFYDWGAGTIVTVSS 117

## RESULT 13

Q924Q1\_MOUSE  
 ID Q924Q1\_MOUSE PRELIMINARY; PRT; 142 AA.  
 AC Q924Q1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE V23-D-J-C mu protein (Fragment).  
 GN Name=AB069917; Synonym=V23-D-J-C mu;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6;  
 RC Kozono Y., Kozono H., Azuma T.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=2499887;  
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;  
 RT "Two murine natural polyreactive autoantibodies are encoded by  
 RT nonmutated germ-line genes."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=3135311;  
 RA Corbet S., Hirm M., Roth C., These J., Fougereau M., Schiff C.;  
 RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of  
 RT C57BL/6 mice by BAUB/c anti-idiotypes stimulates similar strain-  
 RT specific V genes as the original antigen."  
 RL J. Immunol. 141:779-784(1988).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;  
 RA Tillman D.M., Jou N.T., Hill R.D., Marion T.N.;  
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally  
 RT selective B cell stimulation in (NZB x NZW)F1 mice."  
 RL J. Exp. Med. 176:761-779(1992).  
 DR EMBL; AB069913; BAB63929.1; -; mRNA.  
 DR PIR; F33932; F33932.  
 DR PIR; I28833; I28833.  
 DR PIR; PH0985; PH0985.  
 DR PIR; PH1155; PH1155.  
 DR PIR; PH1156; PH1156.  
 DR PIR; PH1157; PH1157.  
 DR PIR; PH1158; PH1158.  
 DR HSSP; P01751; IA6W.  
 DR ENSEMBL; Q924Q1; 1-128.  
 DR MG1; MG1:3576502; AB069917.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT TER 142

Query Match 75.5%; Score 470.5; DB 2; Length 142;  
 Best Local Similarity 75.4%; Pred. No. 2.1e-42;  
 Matches 89; Conservative 11; Mismatches 17; Indels 1; Gaps 1;  
 SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Qy 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYFGNDISY 60  
 Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFTSYIHWIKQTTPGQGLEWVGVIYFGNDISY 60  
 Qy 61 NQKFOGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLRYFDVWGQGTIVTVSS 118  
 Db 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYVCARR-GWEAMDYWGQGTIVTVSS 117

## RESULT 14

Q77MK1\_MOUSE  
 ID Q77MK1\_MOUSE PRELIMINARY; PRT; 470 AA.  
 AC Q77MK1;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein AI324046.  
 GN Name=AI324046;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinaki M.I., Skaleka U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC055910; AAH55910.1; -; mRNA.  
 DR HSSP; P01865; IKB5.  
 DR GO; GO:0003823; F-antigen binding; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003596; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 DR Hypothetical protein; Immunoglobulin domain.  
 KW SEQUENCE 470 AA; 51728 MW; 6D90E4DF896BB090 CRC64;

Query Match 75.5%; Score 470.5; DB 2; Length 470;  
 Best Local Similarity 72.7%; Pred. No. 8.7e-42;

```
Matches 88; Conservative 14; Mismatches 16; Indels 3; Gaps 1;
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTGQGLEWVGVIYPGNDISY 60
Db 20 EVQLQSGPELVKPGASVKISCKASGYTFTGTYMEHWKQSHGSLSEWIGLVNPSNGDTSY 79
QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYYCAR---EVRLRYFDVWGQGTITVTVS 117
Db 80 NQKFGKATLTVDKSSSTAYMELNSLTSDSAVYYCARYYISGSIYFDVWGAGITVTVS 139
QY 118 S 118
Db 140 S 140
RESULT 15
ID HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma
CC making antibodies to the haptan (4-hydroxy-3-nitrophenyl)acetyl
CC (NpB antibodies).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; J00529; AAA38170.1; -; mRNA.
DR PIR; A90809; MHMS18.
DR PDB; 1A6U; X-ray; H=20-139.
DR PDB; 1A6V; X-ray; H/I/J=20-139.
DR PDB; 1A6W; X-ray; H=20-139.
DR PDB; 1NGP; X-ray; H=20-139.
DR PDB; 1NGQ; X-ray; H=20-139.
DR PDB; 1NOB; X-ray; A/C=20-139.
DR Ensembl; ENSMUSG0000063737; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139
FT REGION 20 49
FT REGION 50 54
FT REGION 55 68
FT REGION 69 85
FT REGION 86 117
FT REGION 118 124
FT REGION 125 139
FT DISULFID 41 115
FT NON_TER 139 139
FT STRAND 22 24
Ig heavy chain V region B1-8/186-2.
Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
D segment.
JH2 segment.
By similarity.
```

```
FT STRAND 28 31
FT TURN 33 34
FT STRAND 37 44
FT HELIX 48 50
FT STRAND 52 58
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT HELIX 81 83
FT TURN 84 86
FT STRAND 87 92
FT TURN 93 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 129
FT STRAND 133 137
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
Query Match 75.4%; Score 470; DB 1; Length 139;
Best Local Similarity 74.2%; Pred. No. 2.3e-42;
Matches 89; Conservative 12; Mismatches 17; Indels 2; Gaps 1;
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTGQGLEWVGVIYPGNDISY 60
Db 20 QVQLQPGAEVVKPGASVKLSCKASGYTFTSYMHWKQSHGSLSEWIGRIDPNSGGTQY 79
QY 61 NQKFGKATLTADKSTTAYMQLSLTSDSAVYYCAR---EVRLRYFDVWGQGTITVTVS 118
Db 80 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYYCARYYISGSIYFDVWGQGTITVTVS 139
Search completed: May 9, 2006, 01:32:35
Job time : 109.039 secs
```

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:32:56 ; Search time 26.5628 Seconds  
(without alignments)  
367.271 Million cell updates/sec

Title: US-10-700-632-9  
Perfect score: 623  
Sequence: 1 QVQLQQPGAEVVRPGASVKM.....EVLRLYFDVWGQTTVTSS 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.5	84.2	140	2	US-08-475-815B-11
2	524.5	84.2	470	2	US-09-238-741-4
3	516.5	82.9	140	1	US-08-476-275-6
4	516.5	82.9	140	2	US-08-475-813-6
5	502	80.6	118	2	US-08-766-350B-48
6	501.5	80.5	121	2	US-08-579-378A-7
7	501.5	80.5	121	4	PCT-US93-11612-7
8	501.5	80.5	140	4	PCT-US93-11612-4
9	498	79.9	140	2	US-09-724-138-44
10	495	79.5	140	2	US-09-630-198-44
11	493.5	79.2	140	2	US-08-403-853-18
12	493.5	79.2	140	2	US-08-579-378A-4
13	492	79.0	257	2	US-09-419-788-113
14	490.5	78.7	135	1	US-08-860-174A-4
15	490.5	78.7	274	1	US-08-860-174A-12
16	481.5	77.3	119	2	US-10-194-975-121
17	480.5	77.1	119	1	US-08-553-497A-12
18	479.5	77.0	117	2	US-09-157-370-2
19	478.5	76.8	288	2	US-09-423-439-38
20	478.5	76.8	673	2	US-09-423-439-32
21	474.5	76.2	445	1	US-08-353-400-33
22	474.5	76.2	464	1	US-08-353-400-36
23	473.5	76.0	119	2	US-08-881-037-60
24	473.5	76.0	119	2	US-08-881-037-62
25	473	75.9	117	2	US-09-065-059-15
26	473	75.9	117	2	US-08-913-555-15
27	473	75.9	269	1	US-08-428-257A-72

28	473	75.9	269	1	US-08-491-988-3	Sequence 3, Appli
29	473	75.9	402	1	US-08-491-988-9	Sequence 9, Appli
30	473	75.9	415	1	US-08-491-988-7	Sequence 7, Appli
31	473	75.9	435	1	US-08-491-988-5	Sequence 5, Appli
32	472.5	75.8	119	2	US-08-881-037-63	Sequence 63, Appli
33	472	75.8	122	1	US-08-236-520-9	Sequence 9, Appli
34	472	75.8	122	4	PCT-US95-05262-9	Sequence 9, Appli
35	471.5	75.7	143	1	US-08-236-520-7	Sequence 7, Appli
36	471.5	75.7	143	4	PCT-US95-05262-7	Sequence 7, Appli
37	470.5	75.5	140	1	US-07-946-421-24	Sequence 24, Appli
38	470	75.4	114	2	US-09-344-587-10	Sequence 10, Appli
39	470	75.4	122	2	US-10-092-246-10	Sequence 10, Appli
40	470	75.4	122	2	US-10-092-246-11	Sequence 11, Appli
41	470	75.4	122	2	US-10-096-246A-10	Sequence 10, Appli
42	470	75.4	122	2	US-10-096-246A-11	Sequence 11, Appli
43	469.5	75.4	119	2	US-08-881-037-61	Sequence 61, Appli
44	469	75.3	139	2	US-09-269-921-105	Sequence 105, App
45	468.5	75.2	119	2	US-09-438-954-39	Sequence 39, Appli

## ALIGNMENTS

RESULT 1  
US-08-475-815B-11  
; Sequence 11, Application US/08475815B  
; Patent No. 6399061  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL R.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: LEONARD, JOHN E.  
; APPLICANT: NEWMAN, ROLAND A.  
; APPLICANT: REFF, MITCHELL E.  
; APPLICANT: RASTETER, WILLIAM H.  
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND  
; TITLE OF INVENTION: RADIO-LABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY WINTHROP  
; STREET: 1100 New York Avenue, N.W., Ninth FL.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,815B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,099  
; FILING DATE: 03-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 23522-0157  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 140 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear







```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,350B
FILING DATE: 13-Dec-1996
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-766-350B-48

Query Match      80.6%; Score 502; DB 2; Length 118;
Best Local Similarity 78.8%; Pred. No. 1.2e-39;
Matches 93; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY      1 QVQLQQPGAEVVKPGASVKMSCKASYGTTFTSYIHWIKOTPGGLEWVGVIYPGNDDISY 60
        |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      1 QVQLQQSGNELVRPGASVKMSCKASGYTFTSVMHWKQRPQGGLWIGNLYPENGDTNY 60

QY      61 NQKFGKATLTADKGSSTTAAYMOLSLITSDSAVYYCAREVRLRYFDWGOGTTVTTVSS 118
        |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      61 NQKFGKATLTADTSSSTAAYMOLSLITSDSAVFPCARGXXXGAMDYWGOGTSVTTVSS 118
        |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

```

RESULT 6  
US-08-579-378A-7  
; Sequence 7, Application US/08579378A  
; Patent No. 6210671  
; GENERAL INFORMATION:  
; APPLICANT: Co. Man Sung  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: L-Selectin  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/579,378A  
; FILING DATE: 27-DEC-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/160,074  
; FILING DATE: 30-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/983,946  
; FILING DATE: 01-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95112895.8  
; FILING DATE: 17-AUG-1995

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-579-378A-7

Query Match      80.5%; Score 501.5; DB 2; Length 121;
Best Local Similarity 77.7%; Pred. No. 1.4e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPQGQGLEWGVYIPGNDDISY 60
Db 1 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVMHWKQKPGQGLEWGIYIPYNDGTYK 60

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREV---RLRYFDVWGQGTITVVS 117
Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREYGNVYRFDVWGAGTITVVS 120

QY 118 S 118
Db 121 S 121

RESULT 7
PCT-US93-11612-7
; Sequence 7, Application PC/TUS9311612
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11612
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11612-4

Query Match      80.5%; Score 501.5; DB 2; Length 121;
Best Local Similarity 77.7%; Pred. No. 1.4e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPQGQGLEWGVYIPGNDDISY 60
Db 1 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVMHWKQKPGQGLEWGIYIPYNDGTYK 60

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREV---RLRYFDVWGQGTITVVS 117
Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREYGNVYRFDVWGAGTITVVS 120

QY 118 S 118
Db 121 S 121

RESULT 7
PCT-US93-11612-7
; Sequence 7, Application PC/TUS9311612
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11612
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
```

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11612-7

Query Match      80.5%; Score 501.5; DB 4; Length 121;
Best Local Similarity 77.7%; Pred. No. 1.4e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPQGQGLEWGVYIPGNDDISY 60
Db 1 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVMHWKQKPGQGLEWGIYIPYNDGTYK 60

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREV---RLRYFDVWGQGTITVVS 117
Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYYCAREYGNVYRFDVWGAGTITVVS 120

QY 118 S 118
Db 121 S 121

RESULT 8
PCT-US93-11612-4
; Sequence 4, Application PC/TUS9311612
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11612
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11612-4

Query Match      80.5%; Score 501.5; DB 4; Length 140;
Best Local Similarity 77.7%; Pred. No. 1.6e-39;
Matches 94; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKQTPQGQGLEWGVYIPGNDDISY 60
Db 20 EVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVMHWKQKPGQGLEWGIYIPYNDGTYK 79
```



```
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-403-853-18

Query Match          79.5%; Score 495; DB 1; Length 273;
Best Local Similarity 78.5%; Pred. No. 1.4e-38;
Matches 95; Conservative 10; Mismatches 12; Indels 4; Gaps 2;

QY 1 QVLOQPGAEVVKPGASVMSCKASGYTFTSYIHWIKTPQGGLEWGVVYPGNDDISY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 QVLOQSGAELVKPGASVMSCKASGYTFTSYIHWIKTPQGGLEWIGIFYPGNGDTSY 82
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NOKFOGKATLTADKSTTAYMQLSLTSDSAVYVCARE-VRLRY---FDVWGQGTITTV 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 NOKFKDKATLTADKSTNTAYMQLSLTSDSAVYCARSGGSRYRDGDFYWGQGTITTV 142
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 S 117
Db 143 S 143

RESULT 12
US-08-579-378A-4
; Sequence 4, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschütz, Joe O.
; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-4

Query Match          79.2%; Score 493.5; DB 2; Length 140;
Best Local Similarity 76.9%; Pred. No. 9.1e-39;
Matches 93; Conservative 12; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVMSCKASGYTFTSYIHWIKTPQGGLEWGVVYPGNDDISY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVLOQSGDFDLVKPGASVMSCKASGYTFTSYVHWVWVKQKPGQGLEWIGIYYPYNDGTY 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NOKFOGKATLTADKSTTAYMQLSLTSDSAVYVCAREV---RLRYFDVWGQGTITTVS 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKPKGKATLTADKSSSTAYMELSLTSDSAVYVCAREEYGNVYRVFDMGAGTTTVS 139
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 S 118
Db 140 S 140

RESULT 13
US-09-419-788-113
; Sequence 113, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; TITLE OF INVENTION: Resistance
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
; US-09-419-788-113

Query Match          79.0%; Score 492; DB 2; Length 257;
Best Local Similarity 78.8%; Pred. No. 2.4e-38;
Matches 93; Conservative 10; Mismatches 9; Indels 6; Gaps 1;

QY 1 QVLOQPGAEVVKPGASVMSCKASGYTFTSYIHWIKTPQGGLEWGVVYPGNDDISY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVLOQSGAELVKPGASVMSCKASGYTFTSYNHWVWVKQKPGQGLEWIGIYPRNGDTSY 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NOKFOGKATLTADKSTTAYMQLSLTSDSAVYVCAREVRLRYFDVWGQGTITTVSS 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 63 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARP-----DVMGAGTLLTVSA 114

RESULT 14

US-08-860-174A-4

; Sequence 4, Application US/08860174A  
; Patent No. 5989830  
; GENERAL INFORMATION:  
; APPLICANT: DAVIS, Paul James  
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik  
; APPLICANT: VERHOEIJEN, Martine Elisa  
; APPLICANT: WILSON, Steve  
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT  
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: WASHINGTON, D.C.  
; STATE:  
; COUNTRY: UNITED STATES  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text  
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,174A  
; FILING DATE: June 16, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95307332.7  
; FILING DATE: October 16, 1995  
; APPLICATION NUMBER: PCT/EP/96/03605  
; FILING DATE: August 14, 1996  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-860-174A-4

Query Match 78.7%; Score 490.5; DB 1; Length 135;  
Best Local Similarity 78.0%; Pred. No. 1.7e-38;  
Matches 92; Conservative 10; Mismatches 11; Indels 5; Gaps 1;

Qy 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60

Db 23 QVQLQSGPELVKPGASVKMSCKASGYTFTSYVHWVKQKPGQGLEWIGVIYPNDGTY 82

Qy 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYFDVWGQTTVTVSS 118

Db 83 NEKFKGKATLTSKSSSTAYMQLSSLTSEDSAVVYCSRR-----FDYWGQTTVTVSS 135

RESULT 15

US-08-860-174A-12

; Sequence 12, Application US/08860174A  
; Patent No. 5989830  
; GENERAL INFORMATION:  
; APPLICANT: DAVIS, Paul James  
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik  
; APPLICANT: VERHOEIJEN, Martine Elisa  
; APPLICANT: WILSON, Steve  
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT  
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: WASHINGTON, D.C.  
; STATE:  
; COUNTRY: UNITED STATES  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text  
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,174A  
; FILING DATE: June 16, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95307332.7  
; FILING DATE: October 16, 1995  
; APPLICATION NUMBER: PCT/EP/96/03605  
; FILING DATE: August 14, 1996  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-860-174A-4

; CITY: WASHINGTON, D.C.  
; STATE:  
; COUNTRY: UNITED STATES  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text  
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,174A  
; FILING DATE: June 16, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95307332.7  
; FILING DATE: October 16, 1995  
; APPLICATION NUMBER: PCT/EP/96/03605  
; FILING DATE: August 14, 1996  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-860-174A-12

Query Match 78.7%; Score 490.5; DB 1; Length 274;  
Best Local Similarity 78.0%; Pred. No. 3.6e-38;  
Matches 92; Conservative 10; Mismatches 11; Indels 5; Gaps 1;

Qy 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60

Db 162 QVQLQSGPELVKPGASVKMSCKASGYTFTSYVHWVKQKPGQGLEWIGVIYPNDGTY 221

Qy 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYFDVWGQTTVTVSS 118

Db 222 NEKFKGKATLTSKSSSTAYMQLSSLTSEDSAVVYCSRR-----FDYWGQTTVTVSS 274

Search completed: May 9, 2006, 01:35:40  
Job time : 27.5628 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:57:07 ; Search time 88.6277 Seconds  
(without alignments)  
556.303 Million cell updates/sec

Title: US-10-700-632-9  
Perfect score: 623  
Sequence: 1 QVQLQPGAEVVKPGASVKRM.....EVLRLYFDVWGQTTVTSS 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623	100.0	118	5	US-10-700-632-9
2	613	98.4	118	5	US-10-700-632-7
3	609	97.8	117	5	US-10-700-632-73
4	538.5	86.4	121	4	US-10-366-709-39
5	533.5	85.6	120	4	US-10-366-709-35
6	525.5	84.3	412	4	US-10-013-173-6
7	525.5	84.3	412	4	US-10-150-762-6
8	525.5	84.3	412	4	US-10-244-821-6
9	524.5	84.2	140	4	US-10-238-681-11
10	524.5	84.2	140	4	US-10-411-037-62
11	524.5	84.2	140	4	US-10-411-026-62
12	524.5	84.2	140	4	US-10-410-962-62
13	524.5	84.2	140	4	US-10-411-049-62
14	524.5	84.2	140	4	US-10-327-663-14
15	524.5	84.2	140	4	US-10-410-930-62
16	524.5	84.2	140	4	US-10-410-997-62
17	524.5	84.2	140	4	US-10-411-012-62
18	524.5	84.2	140	4	US-10-287-994-62
19	524.5	84.2	140	4	US-10-410-913-62
20	524.5	84.2	140	5	US-10-723-003-36
21	524.5	84.2	140	5	US-10-410-980-62
22	524.5	84.2	140	5	US-10-410-897-62
23	524.5	84.2	140	5	US-10-492-261-62
24	524.5	84.2	140	6	US-11-004-639-36
25	524.5	84.2	368	5	US-10-880-028-47
26	524.5	84.2	368	5	US-10-880-320-47
27	524.5	84.2	451	5	US-10-822-231-4

28	524.5	84.2	451	5	US-10-822-231-5	Sequence 5, Appli
29	524.5	84.2	470	5	US-10-723-003-40	Sequence 40, Appli
30	524.5	84.2	470	6	US-11-019-180-4	Sequence 4, Appli
31	524.5	84.2	470	6	US-11-004-639-40	Sequence 40, Appli
32	524.5	84.2	626	5	US-10-723-003-44	Sequence 44, Appli
33	524.5	84.2	626	6	US-11-004-639-44	Sequence 44, Appli
34	524.5	84.2	641	5	US-10-723-003-46	Sequence 46, Appli
35	524.5	84.2	641	6	US-11-004-639-46	Sequence 46, Appli
36	524.5	84.2	657	5	US-10-723-003-48	Sequence 48, Appli
37	524.5	84.2	657	6	US-11-004-639-48	Sequence 48, Appli
38	521.5	83.7	423	4	US/10/013	Sequence 8, Appli
39	521.5	83.7	423	4	US/10/150	Sequence 8, Appli
40	521.5	83.7	423	4	US/10/244	Sequence 8, Appli
41	517.5	83.1	121	5	US-10-917-599-1	Sequence 1, Appli
42	516.5	82.9	140	3	US-09-905-928-6	Sequence 6, Appli
43	516.5	82.9	140	4	US-10-096-964-6	Sequence 6, Appli
44	516.5	82.9	140	5	US-10-956-039-6	Sequence 6, Appli
45	512	82.2	122	5	US-10-917-599-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1  
US-10-700-632-9  
; Sequence 9, Application US/10700632  
; Publication No. US20050118183A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunogen, Inc.  
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID  
; FILE REFERENCE: A8427  
; CURRENT APPLICATION NUMBER: US/10/700,632  
; CURRENT FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 60/424,332  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized My9-6 antibody heavy chain variable region  
US-10-700-632-9

Query Match	100.0%	Score 623;	DB 5;	Length 118;
Best Local Similarity	100.0%;	Pred. No. 1.1e-46;		
Matches 118;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60		
Db	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60		
QY	61	NKQFGKATLTADKSTTAYMQLSSTSDSAVYYCAREVRLRYFDVWGQTTVTSS 118		
Db	61	NKQFGKATLTADKSTTAYMQLSSTSDSAVYYCAREVRLRYFDVWGQTTVTSS 118		
RESULT 2				
US-10-700-632-7				
; Sequence 7, Application US/10700632				
; Publication No. US20050118183A1				
; GENERAL INFORMATION:				
; APPLICANT: Immunogen, Inc.				
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID				
; FILE REFERENCE: A8427				
; CURRENT APPLICATION NUMBER: US/10/700,632				
; CURRENT FILING DATE: 2003-11-05				
; PRIOR APPLICATION NUMBER: US 60/424,332				
; PRIOR FILING DATE: 2002-11-07				
; NUMBER OF SEQ ID NOS: 94				

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-7

Query Match      98.4%; Score 613; DB 5; Length 118;
Best Local Similarity 98.3%; Pred. No. 8.4e-46;
Matches 116; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVLOQPQGAEEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGQLEWGVYIPGNDDISY 60
Db 1 QVLOQPQGAEEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGQLEWGVYIPGNDDISY 60
Qy 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYPDVWGQGTITVTVS 118
Db 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYPDVWGQGTITVTVS 118

RESULT 3
US-10-700-632-73
; Sequence 73, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-73

Query Match      97.8%; Score 609; DB 5; Length 117;
Best Local Similarity 98.3%; Pred. No. 1.9e-45;
Matches 115; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVLOQPQGAEEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGQLEWGVYIPGNDDISY 60
Db 1 QVLOQPQGAEEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGQLEWGVYIPGNDDISY 60
Qy 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYPDVWGQGTITVTVS 117
Db 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLRYPDVWGQGTITVTVS 117

RESULT 4
US-10-366-709-39
; Sequence 39, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain A20VH amino acid sequence
US-10-366-709-39

Query Match      85.6%; Score 533.5; DB 4; Length 120;
Best Local Similarity 84.2%; Pred. No. 7.1e-39;
Matches 101; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 2 VQLOQPQGAEEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGQLEWGVYIPGNDDISY 61
Db 1 VQLOQPQGAELVKPGASVKMSCKASGYTFTSYIIHWIKQTPGRLGIEWIGAIYPGNGDTSYN 60
Qy 62 QKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLR---YFDVWGQGTITVTVS 118
Db 61 QKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTYYGCDWYFDVWGQGTITVTVS 120

RESULT 6
US-10-013-173-6
; Sequence 6, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
```

```
; SEQ ID NO 39
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain CA20VH amino acid sequence
US-10-366-709-39

Query Match      86.4%; Score 538.5; DB 4; Length 121;
Best Local Similarity 84.3%; Pred. No. 2.6e-39;
Matches 102; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 1 QVLOQPQGAEEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGQLEWGVYIPGNDDISY 60
Db 1 QVLOQPQGAELVKPGASVKMSCKASGYTFTSYIIHWIKQTPGRLGIEWIGAIYPGNGDTSY 60
Qy 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLR---YFDVWGQGTITVTVS 117
Db 61 NQKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTYYGCDWYFDVWGQGTITVTVS 120

RESULT 5
US-10-366-709-35
; Sequence 35, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain A20VH amino acid sequence
US-10-366-709-35

Query Match      85.6%; Score 533.5; DB 4; Length 120;
Best Local Similarity 84.2%; Pred. No. 7.1e-39;
Matches 101; Conservative 7; Mismatches 9; Indels 3; Gaps 1;

Qy 2 VQLOQPQGAEEVVKPGASVKMSCKASGYTFTSYIIHWIKQTPQGQLEWGVYIPGNDDISY 61
Db 1 VQLOQPQGAELVKPGASVKMSCKASGYTFTSYIIHWIKQTPGRLGIEWIGAIYPGNGDTSYN 60
Qy 62 QKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARVRLR---YFDVWGQGTITVTVS 118
Db 61 QKFGKATLTADKSSSTAYMQLSSLTSEDSAVVYCARSTYYGCDWYFDVWGQGTITVTVS 120

RESULT 6
US-10-013-173-6
; Sequence 6, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
```



APPLICANT: Graves, Scott Stoll  
APPLICANT: Schultz, Joanne Elaine  
APPLICANT: Lin, Yukang  
APPLICANT: Sanderson, James A.  
APPLICANT: Reno, John M.  
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
FILE REFERENCE: 690022.547C1  
CURRENT FILING DATE: 2001-12-07  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 412  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain  
OTHER INFORMATION: antibody-genomic streptavidin fusion  
US-10-013-173-6

Query Match 84.3%; Score 525.5; DB 4; Length 412;  
Best Local Similarity 83.6%; Pred. No. 1.2e-37;  
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYPGNDISY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 128 QVQLVQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKTPGGLEWIGAIYPGNGDTSY 187  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR-----YFDVWGQGTITVTV 116  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 188 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAR-AQLRPNYWYFDVWGAGTTTVT 246  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118  
|||  
Db 247 SS 248  
|||

RESULT 7  
US-10-150-762-6  
Sequence 6, Application US/10150762  
Publication No. US20030103948A1  
GENERAL INFORMATION:  
APPLICANT: Goshorn, Stephen C.  
APPLICANT: Graves, Scott S.  
APPLICANT: Schultz, Joanne E.  
APPLICANT: Lin, Yukang  
APPLICANT: Sanderson, James A.  
APPLICANT: Reno, John M.  
APPLICANT: Dearstynne, Erica A.  
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
FILE REFERENCE: 690022.547C2  
CURRENT FILING DATE: 2002-05-17  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 412  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain  
OTHER INFORMATION: antibody-genomic streptavidin fusion  
US-10-150-762-6

Query Match 84.3%; Score 525.5; DB 4; Length 412;  
Best Local Similarity 83.6%; Pred. No. 1.2e-37;  
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYPGNDISY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 128 QVQLVQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKTPGGLEWIGAIYPGNGDTSY 187  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR-----YFDVWGQGTITVTV 116  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 188 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAR-AQLRPNYWYFDVWGAGTTTVT 246  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118  
|||  
Db 247 SS 248  
|||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR-----YFDVWGQGTITVTV 116  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 188 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAR-AQLRPNYWYFDVWGAGTTTVT 246  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118  
|||  
Db 247 SS 248  
|||

RESULT 8  
US-10-244-821-6  
Sequence 6, Application US/10244821  
Publication No. US20030143233A1  
GENERAL INFORMATION:  
APPLICANT: Goshorn, Stephen Charles  
APPLICANT: Graves, Scott Stoll  
APPLICANT: Schultz, Joanne Elaine  
APPLICANT: Lin, Yukang  
APPLICANT: Sanderson, James Allen  
APPLICANT: Reno, John M.  
APPLICANT: Dearstynne, Erica A.  
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
FILE REFERENCE: 690022.547C3  
CURRENT FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 412  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain  
OTHER INFORMATION: antibody-genomic streptavidin fusion  
US-10-244-821-6

Query Match 84.3%; Score 525.5; DB 4; Length 412;  
Best Local Similarity 83.6%; Pred. No. 1.2e-37;  
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYPGNDISY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 128 QVQLVQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKTPGGLEWIGAIYPGNGDTSY 187  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR-----YFDVWGQGTITVTV 116  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 188 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAR-AQLRPNYWYFDVWGAGTTTVT 246  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118  
|||  
Db 247 SS 248  
|||

RESULT 9  
US-10-238-681-11  
Sequence 11, Application US/10238681  
Publication No. US20030147885A1  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, DARRELL R.  
APPLICANT: HANNA, NABIL  
APPLICANT: LEONARD, JOHN E.  
APPLICANT: NEWMAN, ROLAND A.  
APPLICANT: REFF, MITCHELL E.  
APPLICANT: RASTETTER, WILLIAM H.  
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIO-LABELLED  
TITLE OF INVENTION: ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL  
TITLE OF INVENTION: LYMPHOMA  
FILE REFERENCE: 37003/0291808  
CURRENT FILING DATE: 2002-09-11

Query Match 84.3%; Score 525.5; DB 4; Length 412;  
Best Local Similarity 83.6%; Pred. No. 1.2e-37;  
Matches 102; Conservative 7; Mismatches 8; Indels 5; Gaps 2;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGGLEWVGVIYPGNDISY 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 128 QVQLVQSGAELVKPGASVKMSCKASGYTFTSYNMHWVKTPGGLEWIGAIYPGNGDTSY 187  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR-----YFDVWGQGTITVTV 116  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 188 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAR-AQLRPNYWYFDVWGAGTTTVT 246  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118  
|||  
Db 247 SS 248  
|||



GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DeFrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bowe, Caryn  
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND  
; FILE REFERENCE: 040853-01-5054  
; CURRENT APPLICATION NUMBER: US/10/410,962  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 62  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-410-962-62

Query Match 84.2%; Score 524.5; DB 4; Length 140;  
Best Local Similarity 81.8%; Pred. No. 5.1e-38;  
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;  
  
QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60  
DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 79  
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117  
DB 80 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 139  
QY 118 S 118  
DB 140 A 140

RESULT 13  
US-10-411-049-62  
; Sequence 62, Application US/10411049  
; Publication No. US20040082026A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DeFrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bowe, Caryn  
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
; FILE REFERENCE: 040853-01-5055  
; CURRENT APPLICATION NUMBER: US/10/411,049  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 62  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-411-049-62

Query Match 84.2%; Score 524.5; DB 4; Length 140;  
Best Local Similarity 81.8%; Pred. No. 5.1e-38;  
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;  
  
QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60  
DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 79  
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117  
DB 80 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 139  
QY 118 S 118  
DB 140 A 140

RESULT 14  
US-10-327-663-14  
; Sequence 14, Application US/10327663  
; Publication No. US20040093621A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenya SHITARA  
; APPLICANT: Mikiko SAKURADA  
; APPLICANT: Kazuhisa UCHIDA  
; APPLICANT: Toyohide SHINKAWA  
; APPLICANT: Mitsuo SATOH  
; APPLICANT: Evisuke NAKANO  
; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20  
; FILE REFERENCE: 249-289  
; CURRENT APPLICATION NUMBER: US/10/327,663  
; CURRENT FILING DATE: 2002-12-24  
; PRIOR APPLICATION NUMBER: JP 2001-392753  
; PRIOR FILING DATE: 2001-12-25  
; PRIOR APPLICATION NUMBER: JP 2002-106948  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: JP 2002-319975  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-327-663-14

Query Match 84.2%; Score 524.5; DB 4; Length 140;  
Best Local Similarity 81.8%; Pred. No. 5.1e-38;  
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;  
  
QY 1 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 60  
DB 20 QVLOQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWVGVIYPGNDISY 79  
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTITVTS 117

Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYICARSTYYGGDWYFNVMGAGTTTYS 139  
QY 118 S 118  
Db 140 A 140

RESULT 15  
US-10-410-930-62  
; Sequence 62, Application US/10410930  
; Publication No. US20040115168A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DeFrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bows, Caryn  
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
; TITLE OF INVENTION: BETA  
; FILE REFERENCE: 040853-01-5056  
; CURRENT APPLICATION NUMBER: US/10/410,930  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 62  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-410-930-62

Query Match 84.2%; Score 524.5; DB 4; Length 140;  
Best Local Similarity 81.8%; Pred. No. 5.1e-38;  
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;  
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHIKQTGGGLEWVGVIYPGNDDISY 60  
Db 20 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYTHIKQTGGGLEWVGVIYPGNDDISY 79  
QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYICAREVRLR---YFDVMGAGTTTYS 117  
Db 80 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYICARSTYYGGDWYFNVMGAGTTTYS 139  
QY 118 S 118  
Db 140 A 140

Search completed: May 9, 2006, 02:04:57  
Job time : 88.6277 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:59:22 ; Search time 14.0476 Seconds  
(without alignments)  
388.792 Million cell updates/sec

Title: US-10-700-632-9  
Perfect score: 623  
Sequence: 1 QVQLQPGAEVVKPGASVKM.....EVLRLYFDVWGQTTVTSS 118

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
1: /SIDSS5/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /SIDSS5/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /SIDSS5/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /SIDSS5/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /SIDSS5/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
7: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
8: /SIDSS5/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
9: /SIDSS5/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
10: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
11: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
12: /SIDSS5/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	86.4	121	11	US-11-107-028-35
2	524.5	84.2	140	10	US-11-183-218-62
3	524.5	84.2	140	11	US-11-183-205-62
4	524.5	84.2	451	11	US-11-124-620-5
5	524.5	84.2	451	11	US-11-124-620-7
6	524.5	84.2	451	11	US-11-208-422-25
7	502	80.6	118	11	US-11-126-798-48
8	502	80.6	122	10	US-11-254-138-28
9	502	80.6	122	11	US-11-120-338-7
10	502	80.6	122	11	US-11-106-820-7
11	502	80.6	122	11	US-11-143-077-7
12	502	80.6	122	11	US-11-190-364-7
13	502	80.6	122	11	US-11-147-780-7
14	502	80.6	122	11	US-11-143-386-7
15	502	80.6	122	11	US-11-187-364-7
16	502	80.6	253	11	US-11-106-820-20
17	502	80.6	253	11	US-11-190-364-18
18	502	80.6	253	11	US-11-147-780-18
19	498	79.9	121	11	US-11-107-028-27
20	494.5	79.4	121	11	US-11-107-028-37
21	494	79.3	122	11	US-11-107-028-39

22	492	79.0	118	9	US-10-507-662-30	Sequence 30, Appl
23	492	79.0	118	9	US-10-507-662-31	Sequence 31, Appl
24	489	78.5	118	9	US-10-507-662-36	Sequence 36, Appl
25	483.5	77.6	133	11	US-11-069-834-2	Sequence 2, Appl
26	481.5	77.3	119	11	US-11-054-669-123	Sequence 123, Appl
27	481	77.2	118	9	US-10-507-662-32	Sequence 32, Appl
28	480	77.0	124	9	US-10-932-334-13	Sequence 13, Appl
29	476.5	76.5	121	11	US-11-107-028-38	Sequence 38, Appl
30	476	76.4	118	9	US-10-507-662-33	Sequence 33, Appl
31	476	76.4	123	9	US-10-932-334-88	Sequence 88, Appl
32	476	76.4	123	9	US-10-932-334-92	Sequence 92, Appl
33	475	76.2	118	9	US-10-507-662-35	Sequence 35, Appl
34	475	76.2	118	10	US-11-297-317-2	Sequence 2, Appl
35	475	76.2	448	10	US-11-297-317-4	Sequence 19, Appl
36	471	75.6	116	9	US-10-489-866-19	Sequence 4, Appl
37	470	75.4	120	9	US-10-932-334-72	Sequence 72, Appl
38	470	75.4	122	11	US-11-107-028-41	Sequence 41, Appl
39	469	75.3	120	11	US-11-226-325-198	Sequence 198, Appl
40	469	75.3	120	11	US-11-226-325-201	Sequence 201, Appl
41	469	75.3	122	9	US-10-932-334-73	Sequence 73, Appl
42	469	75.3	139	11	US-11-226-325-4	Sequence 4, Appl
43	468.5	75.2	116	11	US-11-097-812-31	Sequence 31, Appl
44	467	75.0	120	11	US-11-226-325-202	Sequence 202, Appl
45	466.5	74.9	117	9	US-10-932-334-76	Sequence 76, Appl

## ALIGNMENTS

RESULT 1  
US-11-107-028-35  
; Sequence 35, Application US/11107028  
; Publication No. US20050276803A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAN, ANDREW C.  
; APPLICANT: GONG, QIAN  
; APPLICANT: MARTIN, FLAVIUS  
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion  
; FILE REFERENCE: P2112R1  
; CURRENT APPLICATION NUMBER: US/11/107,028  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,263  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 35  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-11-107-028-35

Query Match	86.4%	Score	538.5	DB	11	Length	121
Best Local Similarity	84.3%	Pred. No.	4.1e-36				
Matches	102	Conservative	7	Mismatches	9	Indels	3
Gaps	1						
QY	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHVKOTPGGLEWVGVIYPCNDISY	60				
Db	1	QVQLQPGAEVVKPGASVKMSKASGYTFTSYIHVKOTPGGLEWVGVIYPCNDISY	60				
QY	61	NKQFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---	117				
Db	61	NKQFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR---	117				
QY	118	S	118				
Db	121	S	121				
RESULT 2							
US-11-183-218-62							
; Sequence 62, Application US/11183218							
; Publication No. US2006008906A1							

```
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; FILE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: PCT/US02/032263
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-183-205-62

Query Match      84.2%; Score 524.5; DB 10; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.9e-35;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLGWGVYIPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKQTGPGLEWIGAIYPGNGDTSY 79

Qy 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 139

Qy 118 S 118
Db 140 A 140

RESULT 3
US-11-183-205-62
; Sequence 82, Application US/11/183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01

Query Match      84.2%; Score 524.5; DB 10; Length 140;
Best Local Similarity 81.8%; Pred. No. 5.9e-35;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLGWGVYIPGNDDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYNMHWVKQTGPGLEWIGAIYPGNGDTSY 79

Qy 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 139

Qy 118 S 118
Db 140 A 140

RESULT 4
US-11-124-620-5
; Sequence 5, Application US/11/124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
```

;; PRIOR FILING DATE: 2004-03-26  
;; PRIOR APPLICATION NUMBER: US 10/672,280  
;; PRIOR FILING DATE: 2003-09-26  
;; PRIOR APPLICATION NUMBER: US 10/379,392  
;; PRIOR FILING DATE: 2003-03-03  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 5  
;; LENGTH: 451  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
;; NAME/KEY: misc feature  
;; LOCATION: (243)..(243)  
;; OTHER INFORMATION: Xaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,  
;; OTHER INFORMATION: Glutamine or Threonine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (244)..(244)  
;; OTHER INFORMATION: Xaa can be Valine, Isoleucine or Methionine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (268)..(268)  
;; OTHER INFORMATION: Xaa can be Valine, Isoleucine, Threonine or Tyrosine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (272)..(272)  
;; OTHER INFORMATION: Xaa can be Histidine, Aspartic Acid or Glutamic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (276)..(276)  
;; OTHER INFORMATION: Xaa can be Glutamic Acid or Tyrosine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (278)..(278)  
;; OTHER INFORMATION: Xaa can be Lysine or Glutamic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (301)..(301)  
;; OTHER INFORMATION: Xaa can be Asparagine or Aspartic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (302)..(302)  
;; OTHER INFORMATION: Xaa can be Serine, Alanine or Aspartic Acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (330)..(330)  
;; OTHER INFORMATION: Xaa can be Lysine, Glutamic Acid or Threonine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (334)..(334)  
;; OTHER INFORMATION: Xaa can be Alanine, Tyrosine, Leucine or Isoleucine  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (336)..(336)  
;; OTHER INFORMATION: Xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine  
;; OTHER INFORMATION: or Glutamine  
US-11-124-620-5

Query Match 84.2%; Score 524.5; DB 11; Length 451;  
Best Local Similarity 81.8%; Pred. No. 1.6e-34;  
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;  
  
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKPTPGQGLEWVGVIYPGNDISY 60  
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKPTPGQGLEWVGVIYPGNDISY 60  
  
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117  
DB 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 120

QY 118 S 118  
DB 121 A 121

RESULT 5  
US-11-124-620-7  
;; Sequence 7, Application US/11124620  
;; Publication No. US20060024298A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Lazar, Gregory Alan  
;; APPLICANT: Dang, Wei  
;; APPLICANT: Desjarlais, John R.  
;; APPLICANT: Karki, Sher Bahadur  
;; APPLICANT: Vafa, Omid  
;; APPLICANT: Hayes, Robert  
;; TITLE OF INVENTION: OPTIMIZED FC VARIANTS  
;; FILE REFERENCE: A-71386-9  
;; CURRENT APPLICATION NUMBER: US/11/124,620  
;; CURRENT FILING DATE: 2005-05-05  
;; PRIOR APPLICATION NUMBER: US 60/568,440  
;; PRIOR FILING DATE: 2004-07-15  
;; PRIOR APPLICATION NUMBER: US 60/589,906  
;; PRIOR FILING DATE: 2004-07-20  
;; PRIOR APPLICATION NUMBER: US 60/627,026  
;; PRIOR FILING DATE: 2004-11-09  
;; PRIOR APPLICATION NUMBER: US 60/626,991  
;; PRIOR FILING DATE: 2004-11-10  
;; PRIOR APPLICATION NUMBER: US 60/627,774  
;; PRIOR FILING DATE: 2004-11-12  
;; PRIOR APPLICATION NUMBER: US 10/822,231  
;; PRIOR FILING DATE: 2004-03-26  
;; PRIOR APPLICATION NUMBER: US 10/672,280  
;; PRIOR FILING DATE: 2003-09-26  
;; PRIOR APPLICATION NUMBER: US 10/379,392  
;; PRIOR FILING DATE: 2003-03-03  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn version 3.3  
;; SEQ ID NO 7  
;; LENGTH: 451  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-124-620-7

Query Match 84.2%; Score 524.5; DB 11; Length 451;  
Best Local Similarity 81.8%; Pred. No. 1.6e-34;  
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;  
  
QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKPTPGQGLEWVGVIYPGNDISY 60  
DB 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKPTPGQGLEWVGVIYPGNDISY 60  
  
QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 117  
DB 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYYCAREVRLR---YFDVWGQGTTVTVS 120  
  
QY 118 S 118  
DB 121 A 121

RESULT 6  
US-11-208-423-25  
;; Sequence 25, Application US/11208422  
;; Publication No. US20060067930A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Adams, Camellia W.  
;; APPLICANT: Lien, Samantha  
;; APPLICANT: Lowman, Henry B.  
;; APPLICANT: Marwin, Jonathan S.  
;; APPLICANT: Meng, Yu-Ju G.  
;; TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION  
;; FILE REFERENCE: P2158R1

```
; CURRENT APPLICATION NUMBER: US/11/208,422
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: US 60/603,057
; FILING DATE: 2004-08-19
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-208-422-25

Query Match      84.2%; Score 524.5; DB 11; Length 451;
Best Local Similarity 81.8%; Pred. No. 1.6e-34;
Matches 99; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 S 118
Db 121 A 121

RESULT 7
US-11-126-798-48
; Sequence 48, Application US/11/26798
; Publication No. US20060018895A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; FILER: Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/11/126,798
; FILING DATE: 10-May-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,455
; FILING DATE: 09-May-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20003.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-11-126-798-48

Query Match      80.6%; Score 502; DB 11; Length 118;
Best Local Similarity 78.8%; Pred. No. 3e-33;
Matches 93; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTS 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-11-254-182-28
; Sequence 28, Application US/11/254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 28
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-254-182-28

Query Match      80.6%; Score 502; DB 10; Length 122;
Best Local Similarity 78.7%; Pred. No. 3.1e-33;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QAYLQQSGAEVLRPGASVKMSCKASGYTFTSYIHNIKQTGQGLEWGVYIPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTV 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFGKATLTADKSSSTAYMQLSLTSDSAVYVCAREVRLR---YFDVWGQGTITVTV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118
Db 121 SS 122

RESULT 9
US-11-120-338-7
; Sequence 7, Application US/11/20338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 7
; LENGTH: 122
```



```
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-120-338-7

Query Match      80.6%; Score 502; DB 11; Length 122;
Best Local Similarity 78.7%; Pred. No. 3.1e-33;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR----YFDVWGQGTITV 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVVVYNSYWFYFDVWGQGTITV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118
   ||
Db 121 SS 122

RESULT 10
US-11-106-820-7
; Sequence 7, Application US/111106820
; Publication No. US2006002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-820-7

Query Match      80.6%; Score 502; DB 11; Length 122;
Best Local Similarity 78.7%; Pred. No. 3.1e-33;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR----YFDVWGQGTITV 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVVVYNSYNSYWFYFDVWGQGTITV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118
   ||
Db 121 SS 122

RESULT 11
US-11-143-077-7
; Sequence 7, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
```

```
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-077-7

Query Match      80.6%; Score 502; DB 11; Length 122;
Best Local Similarity 78.7%; Pred. No. 3.1e-33;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR----YFDVWGQGTITV 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVVVYNSYNSYWFYFDVWGQGTITV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118
   ||
Db 121 SS 122

RESULT 12
US-11-190-364-7
; Sequence 7, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 7
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-190-364-7

Query Match      80.6%; Score 502; DB 11; Length 122;
Best Local Similarity 78.7%; Pred. No. 3.1e-33;
Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 1 QVQLQPGAEVVKPGASVKMSCKASGYTFTSYIHWIKOTPGQGLEWVGVIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QAYLQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNDISY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFGKATLTADKSSSTAYMQLSSLTSDSAVYVCAREVRLR----YFDVWGQGTITV 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVVVYNSYNSYWFYFDVWGQGTITV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 SS 118
   ||
Db 121 SS 122

RESULT 13
US-11-147-780-7
; Sequence 7, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
```

; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof

; FILE REFERENCE: P1990R3C1  
; CURRENT APPLICATION NUMBER: US/11/147,780  
; PRIOR FILING DATE: 2005-06-07  
; PRIOR APPLICATION NUMBER: US 60/434,115  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US 60/526,163  
; PRIOR FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: PCT/US03/40426  
; PRIOR FILING DATE: 2003-12-16  
; NUMBER OF SEQ ID NOS: 38

; SEQ ID NO 7

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-147-780-7

Query Match 80.6%; Score 502; DB 11; Length 122;

Best Local Similarity 78.7%; Pred. No. 3.1e-33;

Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60

Db 1 QAYLQDSGAELVRPGASVKMSCKASGYTFTSYNMHWVKOTPRQGLEWIGAIYPGNGDTSY 60

Qy 61 NOKFGKATLTADKSSSTAYMQLSSLTSDSAVYFCAREVRLR----YFDVWGQGTITTV 116

Db 61 NOKFGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVVYYSNSYWFYFDVWGQGTITTV 120

Qy 117 SS 118

Db 121 SS 122

RESULT 14

US-11-143-386-7

; Sequence 7, Application US/11143386

; Publication No. US20060051345A1

; GENERAL INFORMATION:

; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS

; APPLICANT: FROHNA, PAUL A.

; FILE REFERENCE: P2134R1

; CURRENT APPLICATION NUMBER: US/11/143,386

; CURRENT FILING DATE: 2005-06-02

; PRIOR APPLICATION NUMBER: US 60/576,993

; PRIOR FILING DATE: 2004-06-04

; NUMBER OF SEQ ID NOS: 25

; SEQ ID NO 7

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-143-386-7

Query Match 80.6%; Score 502; DB 11; Length 122;

Best Local Similarity 78.7%; Pred. No. 3.1e-33;

Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60

Db 1 QAYLQDSGAELVRPGASVKMSCKASGYTFTSYNMHWVKOTPRQGLEWIGAIYPGNGDTSY 60

Qy 61 NOKFGKATLTADKSSSTAYMQLSSLTSDSAVYFCAREVRLR----YFDVWGQGTITTV 116

Db 61 NOKFGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVVYYSNSYWFYFDVWGQGTITTV 120

Qy 117 SS 118

Db 121 SS 122

RESULT 15

US-11-187-364-7

; Sequence 7, Application US/11187364

; Publication No. US20060062787A1

; GENERAL INFORMATION:

; APPLICANT: Hitraya, Elena

; TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME

; FILE REFERENCE: P2149R1

; CURRENT APPLICATION NUMBER: US/11/187,364

; CURRENT FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US 60/590,302

; PRIOR FILING DATE: 2004-07-22

; NUMBER OF SEQ ID NOS: 36

; SEQ ID NO 7

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-187-364-7

Query Match 80.6%; Score 502; DB 11; Length 122;

Best Local Similarity 78.7%; Pred. No. 3.1e-33;

Matches 96; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

Qy 1 QVQLQQPGAEVVKPGASVKMSCKASGYTFTSYIHNIKOTPGQGLEWGVYIPGNDISY 60

Db 1 QAYLQDSGAELVRPGASVKMSCKASGYTFTSYNMHWVKOTPRQGLEWIGAIYPGNGDTSY 60

Qy 61 NOKFGKATLTADKSSSTAYMQLSSLTSDSAVYFCAREVRLR---YFDVWGQGTITTV 116

Db 61 NOKFGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARVVYYSNSYWFYFDVWGQGTITTV 120

Qy 117 SS 118

Db 121 SS 122

Search completed: May 9, 2006, 02:05:57

Job time : 14.0476 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:21 ; Search time 101.749 Seconds  
(without alignments)  
487.964 Million cell updates/sec

Title: US-10-700-632-10

Perfect score: 586

Sequence: 1 EIVLTQSPGSLAVSPGSRVT.....CHQYLSSRTFGQTKLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- A\_Geneseq\_21:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*
  - 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	586	100.0	113	8 ADO32094	Ado32094 Humanised
2	543	92.7	113	8 ADO32092	Ado32092 Mouse ant
3	543	92.7	114	8 ADO32146	Ado32146 Mouse ant
4	516	88.1	116	9 AEA38741	Aea38741 Murine an
5	516	88.1	667	9 AEA38768	Aea38768 Humanized
6	511	87.2	112	2 AAR54933	Aar54933 MAb 022 V
7	510	87.0	113	9 ADX37184	Adx37184 Murine SM
8	510	87.0	113	9 AEA88701	Aea88701 Mouse ant
9	510	87.0	133	9 ADV92466	Adv92466 Mouse SM5
10	510	87.0	133	9 ADV98529	Adv98529 Novel chi
11	510	87.0	239	9 ADV92470	Adv92470 SM5-1 chi
12	510	87.0	239	9 ADV98533	Adv98533 Novel chi
13	510	87.0	661	9 ADV92490	Adv92490 FL/Fc/chs
14	510	87.0	661	9 ADV98553	Adv98553 Novel chi
15	509	86.9	112	5 AAE23266	Aae23266 S. aureus
16	509	86.9	112	8 ADU33970	Adu33970 Antibody
17	508	86.7	112	5 AAE23264	Aae23264 S. aureus
18	507	86.5	112	5 AAE23270	Aae23270 S. aureus
19	506	86.3	113	7 ADB97820	Adb97820 HBV relat
20	505	86.2	263	2 AAW90226	Aaw90226 Anti-B7.2
21	505	86.2	268	2 AAW90222	Aaw90222 Anti-B7.2
22	505	86.2	268	2 AAW90228	Aaw90228 Anti-B7.1
23	505	86.2	273	2 AAW90224	Aaw90224 Anti-B7.1
24	505	86.2	556	2 AAW90218	Aaw90218 Bispecifi

25	505	86.2	580	2 AAW90217	Aaw90217 Bispecifi
26	503	85.8	112	5 AAE23268	Aae23268 S. aureus
27	503	85.8	244	8 ADG17481	Adg17481 Anti-CD22
28	503	85.8	244	8 ADG17486	Adg17486 Anti-CD22
29	499	85.2	113	2 AAR92215	Aar92215 LL2 Mab V
30	499	85.2	113	2 AAW27695	Aaw27695 Variable
31	499	85.2	113	7 ADC97685	Adc97685 Mouse mon
32	499	85.2	244	8 ADG17479	Adg17479 Anti-CD22
33	499	85.2	244	8 ADG17485	Adg17485 Anti-CD22
34	499	85.2	244	8 ADG17476	Adg17476 Anti-CD22
35	499	85.2	244	8 ADG17478	Adg17478 Anti-CD22
36	499	85.2	272	5 ABG31024	Abg31024 Synthetic
37	499	85.2	272	7 ADD25453	Add25453 Binding d
38	499	85.2	272	7 ADM42728	Adm42728 Synthetic
39	499	85.2	272	9 AEB95396	Aeb95396 Mouse G28
40	499	85.2	272	9 AEB94430	Aeb94430 Mouse ant
41	497	84.8	132	9 AEB08042	Aeb08042 HLA-DR sp
42	497	84.8	238	9 AEB08041	Aeb08041 Murine/hu
43	496	84.6	238	8 ADL23052	Adl23052 Mouse/hum
44	496	84.6	238	8 ADS88793	Ads88793 A mouse/h
45	496	84.6	244	8 ADG17477	Adg17477 Anti-CD22

ALIGNMENTS

RESULT 1

ADO32094

ID ADO32094 standard; protein; 113 AA.

XX AC ADO32094;

XX DT 12-AUG-2004 (first entry)

XX DE Humanised mouse anti-CD33 antibody My9-6 light chain SEQ ID NO:10.

XX KW anti-CD33 antibody; epitope-binding fragment;

KW complementarity-determining region; CDR; immunconjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; humanised;

XX My9-6; light chain.

XX OS Mus musculus.

OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004043344-A2.

XX PD 27-MAY-2004.

XX PF 05-NOV-2003; 2003WO-US032737.

XX PR 07-NOV-2002; 2002US-0424332P.

XX PA (IMMU-) IMMUNOGEN INC.

XX PI Hoffee MG, Tavares D, Lutz RJ;

XX DR WFI; 2004-411619/38.

XX KW New antibodies that bind to CD33, useful for treating a disease

PT associated with CD33 expression, such as myelodysplastic syndrome, acute

PT or chronic myeloid leukemia.

XX PS Claim 14; SEQ ID NO 10; 124pp; English.

XX CC The present invention describes an isolated anti-CD33 antibody or its

CC epitope-binding fragment comprising: (a) at least one complementarity-

CC determining region (CDR); or (b) at least heavy chain variable region

CC comprising 3 CDRs, and at least one light chain variable region, where

CC the CDR has the ability to bind CD33. Also described: (1) an

CC immunconjugate comprising the antibody or its epitope-binding fragment

CC linked to a drug or prodrug; (2) a composition comprising the antibody or

CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment,  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents a humanised mouse anti-CD33 antibody My9-6 light  
 CC chain variable region, which is used in an example from the present  
 CC invention.

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 586; DB 8; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-38;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQQIIPGQSPRLIIYWASTR 60

DB 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQQIIPGQSPRLIIYWASTR 60

QY 61 ESGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

DB 61 ESGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

RESULT 2

AD032092  
 ID AD032092 standard; protein; 113 AA.

XX AC AD032092;

XX DT 12-AUG-2004 (first entry)

XX DE Mouse anti-CD33 antibody My9-6 light chain variable region SEQ ID NO:8.

XX KW anti-CD33 antibody; epitope-binding fragment;  
 KW complementarity-determining region; CDR; immunoconjugate; cytostatic;  
 KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;  
 KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; My9-6;  
 KW light chain.

XX OS Mus musculus.

XX PN WO2004043344-A2.

XX PD 27-MAY-2004.

XX PF 05-NOV-2003; 2003WO-US032737.

XX PR 07-NOV-2002; 2002US-0424332P.

XX PA (IMMU-) IMMUNOGEN INC.

XX PI Hoffee MG, Tavares D, Lutz RJ;

XX WPI; 2004-411619/38.

DR N-PSDB; ADO321139.

XX PT New antibodies that bind to CD33, useful for treating a disease  
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute  
 PT or chronic myeloid leukemia.

XX PS Claim 8; SEQ ID NO 8; 124pp; English.

XX CC The present invention describes an isolated anti-CD33 antibody or its  
 CC epitope-binding fragment comprising: (a) at least one complementarity-  
 CC determining region (CDR); or (b) at least heavy chain variable region  
 CC comprising 3 CDRs, and at least one light chain variable region, where  
 CC the CDR has the ability to bind CD33. Also described: (1) an  
 CC immunoconjugate comprising the antibody or its epitope-binding fragment  
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or  
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment,  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents the mouse anti-CD33 antibody My9-6 light chain  
 CC variable region, which is used in an example from the present invention.

XX SQ Sequence 113 AA;

Query Match 92.7%; Score 543; DB 8; Length 113;

Best Local Similarity 93.8%; Pred. No. 7.4e-35;

Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQQIIPGQSPRLIIYWASTRE 61

DB 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQQIIPGQSPRLIIYWASTRE 61

QY 62 SGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

DB 62 SGVPRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR 113

RESULT 3

AD032146

ID AD032146 standard; protein; 114 AA.

XX AC AD032146;

XX DT 12-AUG-2004 (first entry)

XX DE Mouse anti-CD33 antibody light chain homologous protein SEQ ID NO:62.

XX KW anti-CD33 antibody; epitope-binding fragment;

KW complementarity-determining region; CDR; immunoconjugate; cytostatic;

KW antibody; myelodysplastic syndrome; acute myeloid leukaemia;

KW chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; light chain.

XX OS Mus musculus.

PN W02004043344-A2.  
 XX 27-MAY-2004.  
 XX 05-NOV-2003; 2003WO-US032737.  
 PF 07-NOV-2002; 2002US-0424332P.  
 PR (IMMU-) IMMUNOGEN INC.  
 PA Hoffee MG, Tavares D, Lutz RJ;  
 XX WPI; 2004-411619/38.  
 XX New antibodies that bind to CD33, useful for treating a disease  
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute  
 PT or chronic myeloid leukemia.  
 XX Example 3; SEQ ID NO 62; 124pp; English.  
 XX The present invention describes an isolated anti-CD33 antibody or its  
 CC epitope-binding fragment comprising: (a) at least one complementarity-  
 CC determining region (CDR); or (b) at least one heavy chain variable region  
 CC comprising 3 CDRs, and at least one light chain variable region, where  
 CC the CDR has the ability to bind CD33. Also described: (1) an  
 CC immunoconjugate comprising the antibody or its epitope-binding fragment  
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or  
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical  
 CC composition comprising the immunoconjugate, composition or the antibody  
 CC defined above, or its epitope-binding fragment, and a pharmaceutical  
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,  
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the  
 CC growth of a cell expressing CD33 by contacting the cell with the above  
 CC defined antibody or its epitope-binding fragment, immunoconjugate, or  
 CC (pharmaceutical) composition; (6) determining whether a biological sample  
 CC contains a myelogenous cancer cell; (7) an improved antibody or its  
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated  
 CC polynucleotide encoding the antibody or its epitope-binding fragment  
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy  
 CC chain of the antibody defined above or its epitope-binding fragment; (10)  
 CC a recombinant vector comprising the polynucleotide; (11) a host cell  
 CC transformed with the recombinant vector; (12) producing an antibody or  
 CC its epitope-binding fragment having the ability to bind CD33; and (13)  
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has  
 CC cytostatic activity. The antibody or its epitope-binding fragment  
 CC immunoconjugate, composition can be used for treating a subject having a  
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute  
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.  
 CC It can also be used for inhibiting the growth of cells expressing CD33,  
 CC and for in vivo imaging or as affinity purification agents. The present  
 CC sequence represents a mouse anti-CD33 antibody light chain homologous  
 CC amino acid sequence, which is used in an example from the present  
 CC invention.  
 XX Sequence 114 AA;  
 SQ  
 Query Match 92.7%; Score 543; DB 8; Length 114;  
 Best Local Similarity 93.8%; Pred. No. 7.4e-35;  
 Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 IVLTQSPGSLAVSPGGERVTMSCKSSQSVFFSSQKYNLAWYQIQGPSPLLIYWASTRE 61  
 DB 2 IMLTQSPSSLAVSNGERVTMSCKSSQSVFFSSQKYNLAWYQIQGPSPLLIYWASTRE 61  
 QY 62 SGVPDRFTGSGGDTFTLTSSVQPEDLAIIYCHQYLSRRTFGGKTLEIKR 113  
 DB 62 SGVPDRFTGSGGDTFTLTSSVQPEDLAIIYCHQYLSRRTFGGKTLEIKR 113  
 RESULT 4  
 ID AEA38741  
 XX AEA38741 standard; protein; 116 AA.

AC AEA38741;  
 XX 11-AUG-2005 (first entry)  
 XX Murine anti-TGF-beta antibody (2G7) VL protein, SEQ ID NO: 1.  
 DE Monoclonal antibody; animal disease model; metastasis; cytostatic;  
 XX neoplasm; bone metastases; breast tumor; colorectal tumor; bone disease;  
 KW osteopathic; antibody therapy; radiation therapy; immunotherapy;  
 KW cancer cell proliferation inhibitor;  
 KW transforming growth factor-beta-antagonist; light chain variable region.  
 XX Mus musculus.  
 OS  
 XX Key Location/Qualifiers  
 FH 24..40  
 FT Region /note= "Complementarity determining region (CDR) - L1"  
 FT Region 56..62  
 FT Region /note= "Complementarity determining region (CDR) - L2"  
 FT Region 95..102  
 FT Region /note= "Complementarity determining region (CDR) - L3"  
 XX W02005050200-A2.  
 XX 02-JUN-2005.  
 XX 04-NOV-2004; 2004WO-US036651.  
 XX 13-NOV-2003; 2003US-0520398P.  
 PR 31-MAR-2004; 2004US-0557951P.  
 XX (GETH ) GENENTECH INC.  
 XX Filvaroff EH;  
 XX WPI; 2005-417772/42.  
 XX Screening compounds useful for treating tumor metastasis involves  
 PT administering a test compound to non-human animal model bearing soft  
 PT tissue/bone metastasis and identifying compound that inhibits soft tissue  
 PT growth/bone metastasis.  
 XX Example 2; SEQ ID NO 1; 109pp; English.  
 XX The present invention relates to the screening of candidate molecules  
 CC lanti-transforming growth factor (TGF)-beta antibodies for the treatment  
 CC of tumor metastasis and treatment methods using such molecules. The  
 CC screening method of the invention involves administering several test  
 CC substances to a non-human syngeneic immunocompetent animal model bearing  
 CC at least one soft tissue or bone metastasis optionally in presence of a  
 CC primary tumor, determining the effects of these test substances on the  
 CC soft tissue or bone metastasis and growth of the primary tumor and  
 CC identifying a test substance inhibiting soft tissue growth or bone  
 CC metastasis without adverse effect on the status of the primary tumor. The  
 CC invention is useful in the diagnosis and treatment of breast cancer,  
 CC colorectal cancer, liver and lung metastases, bone destruction and bone  
 CC loss. The animal models of the present invention is useful to screen  
 CC substances useful for the prophylaxis or treatment of soft tissue and/or  
 CC bone metastases which may additionally be effective in treating the  
 CC primary tumor. The present sequence is murine anti-TGF-beta antibody  
 CC (2G7) variable light chain (VL) monoclonal antibody protein.  
 XX Sequence 116 AA;  
 SQ  
 Query Match 88.1%; Score 516; DB 9; Length 116;  
 Best Local Similarity 86.7%; Pred. No. 9.5e-33;  
 Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPGSLAVSPGGERVTMSCKSSQSVFFSSQKYNLAWYQIQGPSPLLIYWASTR 60  
 DB 1 DIMVTQSPSSLAVSNGERVTMSCKSSQSVLYISNQKYNLAWYQIQGPSPLLIYWASTR 60  
 QY 61 ESGVPDRFTGSGGDTFTLTSSVQPEDLAIIYCHQYLSRRTFGGKTLEIKR 113



```

Db      2 IVMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 61
Qy      62 SGVPRDFTGSGGTDFTLTISQVPEDLAIYYCHOYLSSTRTFGQGTGLEIK 112
        |||||
Db      62 SGVPRDFTGSGGTDFTLTISQVPEDLAIYYCHOYLSSTRTFGQGTGLEIK 112
        |||||

RESULT 7
ADX37184
ID      ADX37184 standard; protein; 113 AA.
XX
AC      ADX37184;
XX
XX      21-APR-2005 (first entry)
XX
XX      Murine SM5-1 antibody, mSM5-1, light chain variable region, SEQ ID 4.
XX
XX      Cytostatic; Gene Therapy; light chain variable region; SM5-1; neoplasm;
XX      melanoma; breast tumor; hepatocellular carcinoma.
XX
XX      Mus musculus.
XX
XX      US2005031617-A1.
XX
XX      10-FEB-2005.
XX
XX      26-NOV-2003; 2003US-00722849.
XX
XX      06-JUN-2003; 2003CN-00129123.
XX
XX      23-NOV-2003; 2003CN-01119926.
XX
XX      (MAJJ/) MA J.
XX      (GUOY/) GUO Y.
XX
XX      Ma J, Guo Y;
XX
XX      WPI; 2005-131967/14.
XX      N-PSDB; ADX37188.
XX
XX      New antibody that competitively inhibits the immunospecific binding of a
XX      human SM5-1 specific monoclonal antibody to a SM5-1 target antigen,
XX      PT useful for diagnosing or treating neoplasms, e.g. melanoma or breast
XX      cancer.
XX
XX      Claim 11; SEQ ID NO 4; 40pp; English.
XX
XX      The present invention relates to antibodies which are specific for the
XX      cancer associated antigen SM5-1. The antibodies are useful for assaying
XX      for SM5-1 antigen in a sample, which is useful for the prognosis or
XX      diagnosis of a neoplasm, e.g. melanoma, breast cancer, or hepatocellular
XX      carcinoma. The present sequence is a variable region of one such anti-SM5
XX      -1 antibody.
XX
XX      Query Match 87.0%; Score 510; DB 9; Length 113;
XX      Best Local Similarity 86.6%; Pred. NO. 2.7e-32;
XX      Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy      2 IVTQSPGSLAVSPGERVTMSCKSSQSVFSSQKNYLAWYQQIPGQSPRLIIYWASTRE 61
        |||||
Db      2 IMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 61
        |||||

Qy      62 SGVPRDFTGSGGTDFTLTISQVPEDLAIYYCHOYLSSTRTFGQGTGLEIK 113
        |||||
Db      62 SGVPRDFTGSGGTDFTLTISQVPEDLAIYYCHOYLSSTRTFGQGTGLEIK 113
        |||||

RESULT 8
AEA88701
ID      AEA88701 standard; protein; 113 AA.
XX
XX      AEA88701;
AC

```

```

XX      25-AUG-2005 (first entry)
XX
XX      Mouse anti-SM5-1 antibody light chain variable region, SEQ ID: 4.
XX
XX      cancer; cytostatic; neoplasm; melanoma; breast tumor; endocrine disease;
XX      hepatocellular carcinoma; immunotherapy; light chain variable region;
XX      SM5-1.
XX
XX      Mus sp.
XX
XX      Key Location/Qualifiers
XX      Region 24..40
XX      /note= "Variable region"
XX      Region 56..62
XX      /note= "Variable region"
XX      Region 95..102
XX      /note= "Variable region"
XX
XX      WO2005053604-A2.
XX
XX      16-JUN-2005.
XX
XX      04-JUN-2004; 2004WO-US017855.
XX
XX      06-JUN-2003; 2003CN-00129123.
XX      25-NOV-2003; 2003CN-01119926.
XX      26-NOV-2003; 2003US-00722849.
XX      28-NOV-2003; 2003TW-00133571.
XX
XX      (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX
XX      Ma J, Guo Y;
XX
XX      WPI; 2005-435284/44.
XX      N-PSDB; AEA88705.
XX
XX      New antibody competitively inhibiting immunospecific binding of a human
XX      SM5-1 specific monoclonal antibody to a SM5-1 target antigen, useful in
XX      treating malignancies such as melanoma, breast cancer or hepatocellular
XX      carcinoma.
XX
XX      Claim 11; SEQ ID NO 4; 85pp; English.
XX
XX      The present invention relates to an antibody that competitively inhibits
XX      the immunospecific binding of a human SM5-1 specific monoclonal antibody
XX      (huSM5-1) to a SM5-1 target antigen. The invention is useful in the
XX      fields of cancer biology and immunotherapy, in particular for diagnosing
XX      and treating malignancies such as melanoma, breast cancer or
XX      hepatocellular carcinoma. The present sequence is the mouse anti-SM5-1
XX      antibody light chain variable (VL) region.
XX
XX      Query Match 87.0%; Score 510; DB 9; Length 113;
XX      Best Local Similarity 86.6%; Pred. NO. 2.7e-32;
XX      Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy      2 IVTQSPGSLAVSPGERVTMSCKSSQSVFSSQKNYLAWYQQIPGQSPRLIIYWASTRE 61
        |||||
Db      2 IMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 61
        |||||

Qy      62 SGVPRDFTGSGGTDFTLTISQVPEDLAIYYCHOYLSSTRTFGQGTGLEIK 113
        |||||
Db      62 SGVPRDFTGSGGTDFTLTISQVPEDLAIYYCHOYLSSTRTFGQGTGLEIK 113
        |||||

RESULT 9
ADV92466
ID      ADV92466 standard; protein; 133 AA.
XX
XX      ADV92466;
AC

```

```

DT 10-MAR-2005 (first entry)
XX
DE Mouse SM5-1 (mSM5-1) light chain variable region protein.
XX
KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note="Signal peptide"
FT Region 21..133
FT /note="Light chain variable region gene (VL)"
FT Protein 21..133
FT /note="Mature Mouse SM5-1 (mSM5-1) light chain variable
FT region protein"
XX
XX US2004254108-A1.
PN
XX
XX 16-DEC-2004.
PD
XX
XX 26-NOV-2003; 2003US-00723003.
PF
XX
XX 13-JUN-2003; 2003CN-00129290.
PR
XX 25-NOV-2003; 2003CN-01119930.
PR
XX (MAJU/) MA J.
PA
XX (GUOY/) GUO Y.
PA
XX
XX Ma J, Guo Y;
PI
XX
XX WPI; 2005-030218/03.
DR
XX N-PSDB; ADV92465.
DR
XX
XX New chimeric protein comprises an Flt3 ligand and a proteinous or
XX peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,
XX e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX
XX Example 3; SEQ ID NO 10; 158pp; English.
PS
XX
XX The present invention relates to a chimeric protein having a Flt3 ligand
XX (FL) or its biologically active fragment and a proteinous or peptidyl
XX tumoricidal agent. The invention is useful for treating malignancy,
XX neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a
XX vaccine for eliciting an immune response. The invention is also useful in
XX gene therapy. The present sequence is the mouse SM5-1 (mSM5-1) light
XX chain variable region protein.
XX
XX Sequence 133 AA;
SQ
Query Match 87.0%; Score 510; DB 9; Length 133;
Best Local Similarity 86.6%; Pred. No. 3.1e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 2 IVLTQSPGSLAVSPGKRVMTCKSSQSVFSSQKYNLAYWQIQPSRLLIYWASTRE 61
DB 22 IMWTQSPSLAVSAGEKVTMCKSSQSVLYSSNKNLAYWQKQKPSKLLIYWASTRE 81
QY 62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRFTGQGTKEIKR 113
DB 82 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRFTGQGTKEIKR 133
RESULT 10
ADV98529
ID ADV98529 standard; protein; 133 AA.
XX
XX ADV98529;
XX
XX 24-MAR-2005 (first entry)
DT
XX

```

```

DE Novel chimeric protein-related mSM5-1 light chain protein SeqID10.
XX
KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX
OS Mus sp.
XX
PN WO2005001048-A2.
XX
XX 06-JAN-2005.
PD
XX
XX 04-JUN-2004; 2004WO-US017765.
PF
XX
XX 13-JUN-2003; 2003CN-00129290.
PR
XX 25-NOV-2003; 2003CN-01119930.
PR
XX 26-NOV-2003; 2003US-00723003.
PR
XX 28-NOV-2003; 2003TW-00133577.
PR
XX (SYMB-) SYMBIGENE ACQUISITION CO INC.
PA
XX
XX Ma J, Guo Y;
PI
XX
XX WPI; 2005-075540/08.
DR
XX N-PSDB; ADV98528.
DR
XX
XX New chimeric protein for preventing or treating neoplastic conditions,
XX e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an
XX Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal
XX agent.
XX
XX Example 3; SEQ ID NO 10; 147pp; English.
PS
XX
XX This invention relates to a novel chimeric protein comprising an Flt3
XX ligand, or its biological fragment, and a proteinous or peptidyl
XX tumoricidal agent. The invention may be useful for the production of
XX compounds with a cytostatic activity or a vaccine. The composition and
XX methods are useful for preventing or treating neoplastic conditions, such
XX as melanoma, breast cancer or hepatocellular carcinoma. The present
XX sequence is that of a protein which is related to the chimeric proteins
XX of the invention.
XX
XX Sequence 133 AA;
SQ
Query Match 87.0%; Score 510; DB 9; Length 133;
Best Local Similarity 86.6%; Pred. No. 3.1e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 2 IVLTQSPGSLAVSPGKRVMTCKSSQSVFSSQKYNLAYWQIQPSRLLIYWASTRE 61
DB 22 IMWTQSPSLAVSAGEKVTMCKSSQSVLYSSNKNLAYWQKQKPSKLLIYWASTRE 81
QY 62 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRFTGQGTKEIKR 113
DB 82 SGVPDRFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLSRFTGQGTKEIKR 133
RESULT 11
ADV92470
ID ADV92470 standard; protein; 239 AA.
XX
XX ADV92470;
XX
XX 10-MAR-2005 (first entry)
DT
XX
XX SM5-1 chimeric antibody (ChSM) light chain protein.
DE
XX
XX Antibody engineering; chimeric antibody; cytostatic; gene therapy;
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
KW breast cancer; hepatocellular carcinoma.
XX
XX Homo sapiens.
OS
XX Mus sp.
OS
XX Chimeric.

```



```

XX FH Key Location/Qualifiers
XX FT Peptide 1..20
XX FT Protein /label= Signal peptide
XX FT Protein 21..239
XX FT Protein /note= "Mature SM5-1 chimeric antibody (ChSM) light chain protein"
XX FT Region 21..133
XX FT Region /note= "Light chain variable region gene (VL)"
XX FT Region 134..239
XX FT Region /note= "Human kappa chain constant cDNA (CL)"
XX FN US2004254108-A1.
XX PD 16-DEC-2004.
XX PP 26-NOV-2003; 2003US-00723003.
XX PR 13-JUN-2003; 2003CN-00129290.
XX PR 25-NOV-2003; 2003CN-01119930.
XX PA (MAJJ/) MA J.
XX PA (GUOY/) GUO Y.
XX PI Ma J, Guo Y;
XX PS Example 3; SEQ ID NO 14; 158pp; English.
XX CC The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinous or peptidyl tumoricidal agent. The invention is useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
XX CC Example 3; SEQ ID NO 14; 158pp; English.
XX CC The present invention relates to a chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, such as melanoma, breast cancer or hepatocellular carcinoma. The present sequence is that of a protein which is related to the chimeric proteins of the invention. Note: Two sequences were allocated this SeqID number in the specification, the alternative sequence is shown on page 21.
XX SQ Sequence 239 AA;
Query Match 87.0%; Score 510; DB 9; Length 239;
Best Local Similarity 86.6%; Pred. No. 5.3e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 2 IVLTQSPGSLAVSPGGERVTMSCKSSQSVFSSQKYNLAWYQQIPGQSPRLIIYWASTRE 61
Db 22 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 81
Qy 62 SGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLSRFTFGGTKLEIKR 113
Db 82 SGVPDRFTGSGGTDFTLTISVQAEADLAVIYCHQYFSSYTFGGTKLEIKR 133
RESULT 12
ADV98533
ID ADV98533 standard; protein; 239 AA.
XX AC ADV98533;
XX DT 24-MAR-2005 (first entry)
XX DE Novel chimeric protein-related CHSM light chain protein SeqID14.
XX KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;
XX KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
XX OS Mus sp.
XX OS Synthetic.

```

```

XX WO2005001048-A2.
XX PD 06-JAN-2005.
XX PF 04-JUN-2004; 2004WO-US017765.
XX PR 13-JUN-2003; 2003CN-00129290.
XX PR 25-NOV-2003; 2003CN-01119930.
XX PR 26-NOV-2003; 2003US-00723003.
XX PR 28-NOV-2003; 2003TW-00133577.
XX PA (SYMB-) SYMBIGENE ACQUISITION CO INC.
XX PI Ma J, Guo Y;
XX PS WPI; 2005-075540/08.
XX PR N-PSDB; ADV98532.
XX CC New chimeric protein for preventing or treating neoplastic conditions, e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal agent.
XX CC Example 3; Fig 9; 147pp; English.
XX CC This invention relates to a novel chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, such as melanoma, breast cancer or hepatocellular carcinoma. The present sequence is that of a protein which is related to the chimeric proteins of the invention. Note: Two sequences were allocated this SeqID number in the specification, the alternative sequence is shown on page 21.
XX SQ Sequence 239 AA;
Query Match 87.0%; Score 510; DB 9; Length 239;
Best Local Similarity 86.6%; Pred. No. 5.3e-32;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 2 IVLTQSPGSLAVSPGGERVTMSCKSSQSVFSSQKYNLAWYQQIPGQSPRLIIYWASTRE 61
Db 22 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 81
Qy 62 SGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLSRFTFGGTKLEIKR 113
Db 82 SGVPDRFTGSGGTDFTLTISVQAEADLAVIYCHQYFSSYTFGGTKLEIKR 133
RESULT 13
ADV92490
ID ADV92490 standard; protein; 661 AA.
XX AC ADV92490;
XX DT 10-MAR-2005 (first entry)
XX DE FL/FC/chSMFv fusion protein.
XX KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;
XX KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;
XX KW breast cancer; hepatocellular carcinoma.
XX OS Homo sapiens.
XX OS Mus sp.
XX OS Chimeric.
XX FH Key Location/Qualifiers
XX FT Peptide 1..26
XX FT Protein /label= Signal peptide
XX FT Protein 27..661

```

FT Region /note= "Mature FL/Fc/chSMFv fusion protein"  
 FT 27..182  
 FT /note= "Flt3 ligand extracellular region (FLex)"  
 FT 183..197  
 FT /note= "Hinge region"  
 FT 198..307  
 FT /note= "CH2 region"  
 FT 271  
 FT Misc-difference  
 FT /note= "Encoded by TGC"  
 FT 308..414  
 FT /note= "CH3 region"  
 FT 415..533  
 FT /note= "Heavy chain variable region gene (VH)"  
 FT 534..556  
 FT /note= "Linker region"  
 FT 557..661  
 FT /note= "Light chain variable region gene (VL)"  
 XX  
 PN US2004254108-A1.  
 XX  
 PD 16-DEC-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723003.  
 XX  
 PR 13-JUN-2003; 2003CN-00129290.  
 PR 25-NOV-2003; 2003CN-01119930.  
 XX  
 PA (MAJJ/) MA J.  
 PA (GUOY/) GUO Y.  
 XX  
 PI Ma J, Guo Y;  
 XX  
 XX WPI; 2005-030218/03.  
 DR N-PSDB; ADV92489.  
 XX  
 XX New chimeric protein comprises an Flt3 ligand and a proteinous or  
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
 XX  
 PS Claim 23; SEQ ID NO 34; 158pp; English.  
 XX  
 CC The present invention relates to a chimeric protein having a Flt3 ligand  
 CC (FL) or its biologically active fragment and a proteinous or peptidyl  
 CC tumoricidal agent. The invention is useful for treating malignancy,  
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma, and as a  
 CC vaccine for eliciting an immune response. The invention is also useful in  
 CC gene therapy. The present sequence is the FL/Fc/chSMFv fusion protein.  
 XX  
 SQ Sequence 661 AA;  
 Query Match 87.0%; Score 510; DB 9; Length 661;  
 Best Local Similarity 86.6%; Pred. No. 1.3e-31;  
 Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 I VLTQSPGSLAVSPGKRVMTCSKSSQSVFSSQKNYLAWYQQIPGQSPRLIYWASTRE 61  
 DB 550 I MWTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 609  
 QY 62 SGVPRFTGSGSGTDFLTITSSVQPEDLAIIYVCHQYLSRRTFGQGTKEIKR 113  
 DB 610 SGVPRFTGSGSGTDFLTITSSVQAEADLAIVYCHQYVFSSTFGGTKEIKR 661  
 RESULT 14  
 ADV98553  
 ID ADV98553 standard; protein; 661 AA.  
 XX  
 AC ADV98553;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Novel chimeric protein-related FL/Fc/chSMFv protein SeqID34.  
 XX

KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO2005001048-A2.  
 XX  
 PD 06-JAN-2005.  
 XX  
 PF 04-JUN-2004; 2004WO-US017765.  
 XX  
 PR 13-JUN-2003; 2003CN-00129290.  
 PR 25-NOV-2003; 2003CN-01119930.  
 PR 26-NOV-2003; 2003US-00723003.  
 PR 28-NOV-2003; 2003TW-00133577.  
 XX  
 PA (SYMB-) SYMBIGENE ACQUISITION CO INC.  
 XX  
 PI Ma J, Guo Y;  
 XX  
 DR WPI; 2005-075540/08.  
 DR N-PSDB; ADV98552.  
 XX  
 XX New chimeric protein for preventing or treating neoplastic conditions,  
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an  
 PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal  
 PT agent.  
 XX  
 PS Claim 23; SEQ ID NO 34; 147pp; English.  
 XX  
 CC This invention relates to a novel chimeric protein comprising an Flt3  
 CC ligand, or its biological fragment, and a proteinous or peptidyl  
 CC tumoricidal agent. The invention may be useful for the production of  
 CC compounds with a cytostatic activity or a vaccine. The composition and  
 CC methods are useful for preventing or treating neoplastic conditions, such  
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present  
 CC sequence is that of a protein which is related to the chimeric proteins  
 CC of the invention.  
 XX  
 SQ Sequence 661 AA;  
 Query Match 87.0%; Score 510; DB 9; Length 661;  
 Best Local Similarity 86.6%; Pred. No. 1.3e-31;  
 Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 I VLTQSPGSLAVSPGKRVMTCSKSSQSVFSSQKNYLAWYQQIPGQSPRLIYWASTRE 61  
 DB 550 I MWTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRE 609  
 QY 62 SGVPRFTGSGSGTDFLTITSSVQPEDLAIIYVCHQYLSRRTFGQGTKEIKR 113  
 DB 610 SGVPRFTGSGSGTDFLTITSSVQAEADLAIVYCHQYVFSSTFGGTKEIKR 661  
 RESULT 15  
 AAE29266  
 ID AAE29266 standard; protein; 112 AA.  
 XX  
 AC AAE29266;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.  
 XX  
 KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;  
 KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;  
 KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 FH Key Location/Qualifiers

FT Region 24. .40  
FT /note= "CDR1"  
FT 56. .62  
FT /note= "CDR2"  
FT 95. .102  
FT /note= "CDR3"  
XX  
PN WO200272600-A2.  
XX  
XX  
PD 19-SEP-2002.  
XX  
XX  
PF 28-JAN-2002; 2002WO-US002296.  
XX  
XX 26-JAN-2001; 2001US-0264072P.  
PR 12-MAR-2001; 2001US-0274611P.  
PR 18-JUN-2001; 2001US-0298413P.  
PR 30-JUL-2001; 2001US-0308116P.  
XX  
XX (INHI-) INHIBITEX INC.  
XX  
XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;  
XX  
XX WPI; 2002-759834/82.  
DR N-PSDB; AAD46865.  
XX  
XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for  
PT treating or preventing Staphylococcus aureus infection e.g. wound  
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis in  
PT a human or animal.  
XX  
XX Claim 11; Page 35; 80pp; English.  
XX  
XX The invention relates to monoclonal antibody which binds the clumping  
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA  
CC monoclonal antibody is useful for treating or preventing S. aureus  
CC infection in a human or animal, and for inhibiting the binding of  
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment  
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3  
CC protein is useful for inducing an immunological response in a human or  
CC animal. These staphylococcal infections include wound infections, sepsis,  
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The  
CC present sequence is Staphylococcus aureus ClfA specific monoclonal  
CC antibody 12-9VLA-1 (variable light sequence) protein  
XX  
XX Sequence 112 AA;  
SQ  
  
Query Match 86.9%; Score 509; DB 5; Length 112;  
Best Local Similarity 87.4%; Pred. No. 3.2e-32;  
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 2 IVLTQSPGSLAVSPGERVTWCKSSQSVFSSSKYNYLAWYQQIPGQSPRLIIYWASTRE 61  
Db 2 IMMTQSPSSSLAVSAGEKVTWCKSSQSVLYSSNKNYLAAYQQIPGQSPKLLIYWASTRE 61  
  
Qy 62 SGVPDRFTGSGGTDFTLTITSSVQPEDLAIYYCHQYLSSRTFGQGTKLEIK 112  
Db 62 SGVPDRFTGSGGTDFTLTITSSVQAEADLVNYYCHQYLSSVTFGGGTKLEIK 112  
  
Search completed: May 9, 2006, 01:25:26  
Job time : 103.749 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:25:51 ; Search time 17.1212 Seconds  
(without alignments)  
635.031 Million cell updates/sec

Title: US-10-700-632-10  
Perfect score: 586  
Sequence: 1 EIVLTQSPGSLAVSPGSRVT.....CHQYLSRTRFGQGTKLEIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	83.6	111	2 G30502	Ig kappa chain V r
2	478	81.6	112	2 S41393	Ig kappa chain V r
3	477	81.4	118	2 P70356	Ig kappa chain V r
4	473	80.7	138	2 S26040	Ig kappa chain pre
5	471	80.4	103	2 PH1054	Ig kappa chain V r
6	469.5	80.1	113	2 S34002	Ig kappa chain V r
7	467	79.7	112	2 S09970	Ig kappa chain V-J
8	467	79.7	112	2 S43103	Ig kappa chain V-J
9	467	79.7	133	2 P50023	Ig kappa chain pre
10	465.5	79.4	114	1 K4HULN	Ig kappa chain V-I
11	463.5	79.1	145	2 PL0014	Ig kappa chain pre
12	462	78.8	112	2 PL0265	Ig kappa chain V r
13	461.5	78.8	120	2 S51147	antibody light cha
14	461.5	78.8	240	2 S06084	Ig kappa chain pre
15	460	78.5	113	2 P70407	Ig light chain V r
16	460	78.5	133	1 K4HUUI	Ig kappa chain pre
17	459	78.3	101	2 S26337	Ig kappa chain pre
18	457.5	78.1	134	2 S49531	anti-Sm antibody V
19	455.5	77.7	134	2 PC1214	Ig kappa chain pre
20	451	77.0	138	2 A53261	Ig kappa chain pre
21	447.5	76.4	113	2 S30520	Ig kappa chain V r
22	447.5	76.4	113	2 S34003	Ig kappa chain V r
23	447.5	76.4	220	2 A31790	Ig kappa chain pre
24	444.5	75.9	113	2 A49260	antitumor monoclon
25	444.5	75.9	134	1 K4HU17	Ig kappa chain pre
26	443.5	75.7	133	2 PL0263	Ig kappa chain V r
27	443.5	75.7	132	2 S46373	Ig kappa chain V-J
28	442.5	75.5	113	2 JC2270	PL7-6 antibody lig
29	442	75.4	113	2 PT0408	Ig light chain V r

30	441.5	75.3	113	2 S30523	Ig kappa chain V r
31	436.5	74.5	135	2 S38807	Ig light chain V-J
32	436.5	74.5	214	2 S68212	Ig kappa chain (Ma
33	436	74.4	104	2 PH1102	Ig light chain V r
34	435	74.2	104	2 PH1101	Ig light chain V r
35	433.5	74.0	112	2 F30538	Ig kappa chain V r
36	433.5	74.0	129	2 S40347	Ig kappa chain - h
37	432.5	73.8	112	2 S30538	Ig kappa chain V r
38	432.5	73.8	114	2 S44116	Ig kappa chain V-J
39	432	73.7	104	2 PH1104	Ig light chain V r
40	431.5	73.6	114	2 S44119	Ig kappa chain V-J
41	430	73.4	103	2 PH1050	Ig light chain V r
42	430	73.4	109	2 G30601	Ig kappa chain V-I
43	429	73.2	104	2 PH1103	Ig light chain V r
44	428	73.0	129	2 S49532	anti-Sm antibody V
45	427.5	73.0	113	2 PL0264	Ig kappa chain V r

ALIGNMENTS

RESULT 1

G30502  
Ig kappa chain V region (A52) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Nov-1988 #sequence\_revision 03-Nov-1988 #text\_change 21-Jan-2000  
C:Accession: G30502  
R:Elilat, D.; Webster, D.M.; Rees, A.R.  
J. Immunol. 141, 1745-1753, 1988  
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 ml  
A:Reference number: A30502; MUID:88315787; PMID:2457627  
A:Accession: G30502  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-111 <EIL>  
A:Cross-references: UNIPARC:UPI0000176AF0  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 490; DB 2; Length 111;  
Best Local Similarity 84.5%; Pred. No. 7.5e-35;  
Matches 93; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy	2	I V L T Q S P G S L A V S P G R V T W S C K S S Q S V F F S S S Q N Y L A W Y Q Q I P G S P R L I I Y W A S T R E	61
Db	2	I M M T Q S P S S L A V A G E K V T W S C K S S Q S V L Y S S Q N Y L A W Y Q Q K P G S P K L I I Y W A S T R E	61
Qy	62	S G V P D R F T G S G S G D F T L T I S S V Q P E D L A I Y Y C H Q Y L S S R T F G Q G T K L E I	111
Db	62	S G V P D R F T G S G S G D F T L T I S S V Q A E D L A V Y Y C H Q F S S W T F G G T K L E I	111

RESULT 2

S41393  
Ig kappa chain V region (12.5H VL) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001  
C:Accession: S41393  
R:Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.  
submitted to the EMBL Data Library, January 1994  
A:Description: Structural characterization of an (NZB X NZW) F1 mouse-derived IgM anti-1-  
A:Reference number: S41393  
A:Accession: S41393  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <MAR>  
A:Cross-references: UNIPARC:UPI000176CCB; EMBL:Z29536  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 81.6%; Score 478; DB 2; Length 112;

```

F;41-121/Domain: immunoglobulin homology <IMM>

Query Match      80.7%; Score 473; DB 2; Length 138;
Best Local Similarity 77.9%; Pred.No.2.5e-33;
Matches 88; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY    1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVPFFSSQKNYLAWYQQIPGOSPRLLIYWASTR 60
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     26 DIVMSQPSLSLTVSVEKVTMNCKSQSLYSNNQKNYLAWYQOKPGQSPKLLIYWASTR 85
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    61 ESGVDRFTGSGSGTDFTLTISSVQPEDLAIIYCHYLSRTFGQGFKLIKR 113
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     86 ESGVDRFTGSGSGTDFTLTISSVKAEADLAVYFCQQYYSLTFAGATKLKLR 138
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 5
PHI054
IG light chain V region (clone 202.135) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1054
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and IgG anti-DNA antibodies are the products of clonally selected B cells
A;Reference number: PH0971; PMID:92381444; PMID:1512540
A;Accession: PH1054
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPARC:UPI0000176AAE
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 471; DB 2; Length 103;
Best Local Similarity 87.3%; Pred.No.2.8e-33;
Matches 89; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY    2 IVLTQSPGSLAVSPGERVTMSCKSSQSVPFFSSQKNYLAWYQQIPGOSPRLLIYWASTRE 61
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     2 IMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQOKPGQSPKLLIYWASTRE 61
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    62 SGVDPDRFTGSGSGTDFTLTISSVQPEDLAIIYCHYLSRTFF 103
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     62 SGVDPDRFTGSGSGTDFTLTISSVQAEDLAVVYCHYLSSTVF 103
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 6
S34002
IG kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34002; S30522
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal antibodies specific for human IgG1
A;Reference number: S34001; PMID:93209281; PMID:7681398
A;Accession: S34002
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <MAR>
A;Cross-references: UNIPARC:UPI0000176D32; EMBL:Z18328
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match      80.1%; Score 469.5; DB 2; Length 113;
Best Local Similarity 78.8%; Pred.No.4.1e-33;
Matches 89; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY    1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVPFFSSQKNYLAWYQQIPGOSPRLLIYWASTR 60
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

Db 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAHYQKPGQPPKLLIYWASTR 60  
QY 61 ESGVDPDRFTGSGGTDFLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIK 112  
Db 61 ESGVDPDRFTGSGGTDFLTITSSVQPEDLAIIYCHQYIGYIPRTFGQGTKEIK 113

RESULT 7  
S09970  
Ig kappa chain V-J region (4C8) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000  
C/Accession: S09970  
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
Eur. J. Immunol. 20, 771-777, 1990  
A/Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
A/Reference number: S09955; MUID:90269328; PMID:2347362  
A/Accession: S09970  
A/Molecule type: mRNA  
A/Residues: 1-112 <REI>  
A/Cross-references: UNIPARC:UPI0000115E69; EMBL:X51858; NID:G55406; PIDN:CAA36151.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 467; DB 2; Length 112;  
Best Local Similarity 77.7%; Pred. No. 6.7e-33;  
Matches 87; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQPGQSPRLLIYWASTR 60  
Db 1 DIVMSQSPSSLTSGVGEKVTMCKSSQSLNYSNNKNYLAHYQKPGQSPKLLIYWASTR 60

QY 61 ESGVDPDRFTGSGGTDFLTITSSVQPEDLAIIYCHQYLSRTFGQGTKEIK 112  
Db 61 ESGVDPDRFTGSGGTDFLTITSSVQAEADLAIVYFQQYSSLTFGGKLEIK 112

RESULT 8  
S43103  
Ig kappa chain V-J region (4B1 VL) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 24-May-2001  
C/Accession: S43103  
R;Gilbert, D.; Brard, F.; Margartte, C.; Delpach, A.; Tron, F.  
submitted to the EMBL Data Library, March 1994  
A/Description: An idotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody  
A/Reference number: S42484  
A/Accession: S43103  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-112 <GL>  
A/Cross-references: UNIPARC:UPI0000116626; EMBL:X31353; NID:G467574; PIDN:CAA83231.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 467; DB 2; Length 112;  
Best Local Similarity 80.4%; Pred. No. 6.7e-33;  
Matches 90; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQPGQSPRLLIYWASTR 60  
Db 1 DIVMSQSPSSLTSGVGEKVTMCKSSQSLNYSNNKNYLAHYQKPGQSPKLLIYWASTR 60

QY 61 ESGVDPDRFTGSGGTDFLTITSSVQPEDLAIIYCHQYLSRTFGQGTKEIK 112  
Db 61 ESGVDPDRFTGSGGTDFLTITSSVQAEADLAIVYCKQSYNLTFGGKLEIK 112

RESULT 9  
PS0023  
Ig kappa chain precursor V region (6A4) - mouse

C/Species: Mus musculus (house mouse)  
C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C/Accession: PS0023  
R;Margat, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.  
Gene 74, 335-345, 1988  
A/Title: Cloning and characterization of cDNAs coding for the heavy and light chains of  
A/Reference number: PS0023; MUID:89232725; PMID:3149944  
A/Accession: PS0023  
A/Molecule type: mRNA  
A/Residues: 1-133 <MAR>  
A/Cross-references: UNIPARC:UPI0000176787  
A/Experimental source: strain BALB/c  
A/Note: the amino-terminal four residues of the mature protein were directly sequenced  
C/Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>  
F;36-116/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 467; DB 2; Length 133;  
Best Local Similarity 79.6%; Pred. No. 7.9e-33;  
Matches 90; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQPGQSPRLLIYWASTR 60  
Db 21 DIVMSQSPSSLTSGVGEKVTMCKSSQSLNYSNNKNYLAHYQKPGQSPKLLIYWASTR 80

QY 61 ESGVDPDRFTGSGGTDFLTITSSVQPEDLAIIYCHQYLSRTFGQGTKEIKR 113  
Db 81 ESGVDPDRFTGSGGTDFLTITSSVQAEADLAIVYCKQSYNLTFGGKLEIKR 133

RESULT 10  
K4HULN  
Ig kappa chain V-IV region (Len) - human  
C/Species: Homo sapiens (man)  
C/Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 01-Dec-2000  
C/Accession: A01903; F61458  
R;Schneider, M.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975  
A/Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe IV  
A/Reference number: A01903; MUID:76004342; PMID:50995  
A/Accession: A01903  
A/Molecule type: protein  
A/Residues: 1-114 <SCH>  
A/Cross-references: UNIPARC:UPI0000173708  
A/Note: this is the first completely sequenced V region of a new kappa chain subgroup,  
A/Note: the C region of this chain has the Inv (3) marker  
R;Brouet, J.C.; Bellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A/Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-ass  
A/Reference number: A61458; MUID:90039128; PMID:2478651  
A/Accession: F61458  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <BRO>  
A/Cross-references: UNIPARC:UPI0000173709  
C/Comment: This is a Bence Jones protein.  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IGA and IgM, the subunits associate into 1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>  
F;23-94/Disulfide bonds: #status predicted

Query Match 79.4%; Score 465.5; DB 1; Length 114;  
Best Local Similarity 78.1%; Pred. No. 9.1e-33;  
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAHYQIQPGQSPRLLIYWASTR 60  
Db 1 DIVMTQSPNSLAVSLGERATINCKSSQSVLYSSNNKNYLAHYQKPGQPPKLLIYWASTR 60





Search completed: May 9, 2006, 01:33:50  
Job time : 18.1212 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:18:41 ; Search time 103.461 Seconds  
(without alignments)

770.577 Million cell updates/sec

Title: US-10-700-632-10

Perfect score: 586

Sequence: 1 E1VLQSPGSLAVSPGSRVT.....CHQVLSRTFGQGTLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464.5	79.3	114	1 KV4A HUMAN	P01625 homo sapien
2	460	78.5	133	1 KV4B HUMAN	P06313 homo sapien
3	457.5	78.1	134	1 KV4C HUMAN	P06314 homo sapien
4	452.5	77.2	240	2 Q52L64 MOUSE	Q52L64 mus musculus
5	433.5	74.0	255	2 Q6KB05 MOUSE	Q6KB05 mus musculus
6	425	72.5	129	1 KV3L HUMAN	P18135 homo sapien
7	420	71.7	121	1 KV40 HUMAN	P06312 homo sapien
8	417	71.2	109	1 KV3E HUMAN	P01623 homo sapien
9	415	70.8	109	1 KV3B HUMAN	P01620 homo sapien
10	414	70.6	129	1 KV3M HUMAN	P18136 homo sapien
11	413	70.5	109	1 KV3D HUMAN	P01622 homo sapien
12	412	70.3	109	2 Q9UL78 HUMAN	Q9UL78 homo sapien
13	406.5	69.4	109	1 KV4D HUMAN	P83593 homo sapien
14	406.5	69.4	236	2 Q6PIE8 HUMAN	Q6PIE8 homo sapien
15	404	68.9	109	1 KV3G HUMAN	P04206 homo sapien
16	395.5	67.5	236	2 Q6P5E8 HUMAN	Q6P5E8 homo sapien
17	393	67.1	108	1 KV3A HUMAN	P01619 homo sapien
18	392	66.9	109	2 Q9UL86 HUMAN	Q9UL86 homo sapien
19	389	66.4	235	2 Q6PJF2 HUMAN	Q6PJF2 homo sapien
20	385	65.7	235	2 Q6GMV9 HUMAN	Q6GMV9 homo sapien
21	383	65.4	129	1 KV3H HUMAN	P04207 homo sapien
22	382.5	65.3	128	1 KV3K HUMAN	P06311 homo sapien
23	382	65.2	109	1 KV3F HUMAN	P01624 homo sapien
24	382	65.2	235	2 Q6GMW0 HUMAN	Q6GMW0 homo sapien
25	375.5	64.1	108	2 Q9UL70 HUMAN	Q9UL70 homo sapien
26	375	64.0	109	2 Q9UL85 HUMAN	Q9UL85 homo sapien
27	372.5	63.6	240	2 Q6PIH6 HUMAN	Q6PIH6 homo sapien
28	371.5	63.4	108	1 KV1M HUMAN	P01605 homo sapien
29	371.5	63.4	108	2 Q9UL83 HUMAN	Q9UL83 homo sapien
30	369	63.0	107	2 Q96SA9 HUMAN	Q96SA9 homo sapien
31	368.5	62.9	234	2 Q569I9 HUMAN	Q569I9 homo sapien

32	367.5	62.7	108	1 KV1V HUMAN	P04430 homo sapien
33	367.5	62.7	108	2 Q9UL77 HUMAN	Q9UL77 homo sapien
34	367	62.6	239	2 Q8NEK0 HUMAN	Q8NEK0 homo sapien
35	365.5	62.4	108	2 Q9UL79 HUMAN	Q9UL79 homo sapien
36	365.5	62.4	114	1 KV1A MOUSE	P01632 mus musculus
37	365.5	62.0	100	1 KV3C HUMAN	P01621 homo sapien
38	362.5	61.9	108	1 KV1H HUMAN	P01600 homo sapien
39	362.5	61.9	238	2 Q58EU4 MOUSE	Q58EU4 mus musculus
40	361.5	61.7	236	2 Q6PIT5 HUMAN	Q6PIT5 homo sapien
41	359.5	61.3	108	1 KV1K HUMAN	P01603 homo sapien
42	359	61.3	110	1 KV3P MOUSE	P01668 mus musculus
43	358	61.1	117	1 KV2E HUMAN	P06309 homo sapien
44	356.5	60.8	129	1 KV1W HUMAN	P04431 homo sapien
45	356.5	60.8	236	2 Q6PIH7 HUMAN	Q6PIH7 homo sapien

#### ALIGNMENTS

#### RESULT 1

KV4A\_HUMAN STANDARD; PRT; 114 AA.  
AC P01625;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-IV region Len.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=76004342; PubMed=50995;  
RA Schneider M., Hilschmann N.;  
RT "The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len).";  
RT Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
RN [2]  
RP SEQUENCE REVISION TO 9.  
RA Salomon A.;  
RL Submitted (AUG-1996) to Swiss-Prot.  
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

-----  
CC PDB; 1EEQ; X-ray; A/B=1-114.  
DR PDB; 1EEU; X-ray; A/B=1-114.  
DR PDB; 1EFQ; X-ray; A=1-114.  
DR PDB; 1EK3; X-ray; A/B=1-114.  
DR PDB; 1LVE; X-ray; @=1-114.  
DR PDB; 2LVE; X-ray; @=1-114.  
DR PDB; 3LVE; X-ray; @=1-114.  
DR PDB; 4LVE; X-ray; A/B=1-114.  
DR PDB; 5LVE; X-ray; A=1-114.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.  
KW Framework-1.  
FT REGION 1 23 Complementarity-determining-1.  
FT REGION 24 40 Framework-2.  
FT REGION 41 55 Framework-2.

```

FT REGION 56 62 Complementarity-determining-2.
FT REGION 63 94 Framework-3.
FT REGION 95 101 Complementarity-determining-3.
FT REGION 102 113 Complementarity-determining-4.
FT DISULFID 23 94 By similarity.
FT NON_TER 114 114
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT STRAND 30 31
FT TURN 32 35
FT STRAND 36 37
FT STRAND 39 44
FT TURN 46 47
FT STRAND 51 55
FT TURN 56 58
FT STRAND 59 60
FT TURN 62 63
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 75
FT STRAND 76 81
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 79.3%; Score 464.5; DB 1; Length 114;
Best Local Similarity 78.1%; Pred. No. 2.8e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIVLTQSPGSLAVSPGGERVTMSCKSSQVFFSSQKKNLYAWYQQIPGQSPRLIIYWASTR 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSNSKNLYAWYQQKPGQPPLIIYWASTR 60

QY 61 ESGVPRDRTGSGSGTDFTLTISVQPEDLAIVYCHQYLSS-RTFGQGTKLEIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVPRDRTGSGSGTDFTLTISVQPEDLAIVYCHQYLSS-RTFGQGTKLEIKR 114

RESULT 2
KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region J1 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene.";
RL Nucleic Acids Res. 13:6515-6529 (1985).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; Z00022; CAA77317.1; -; Genomic_DNA.
DR PIR; A01904; K4HUIJ.
DR HSSP; P01625; ILVE.

```

```

DR SMR; P06313; 21-133.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-IV region J1.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 122 Complementarity-determining-3.
FT REGION 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14633 MW; 5FB3953066744AF4 CRC64;

Query Match 78.5%; Score 460; DB 1; Length 133;
Best Local Similarity 77.0%; Pred. No. 9.8e-40;
Matches 87; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGGERVTMSCKSSQVFFSSQKKNLYAWYQQIPGQSPRLIIYWASTR 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSNSKNLYAWYQQKPGQPPLIIYWASTR 80

QY 61 ESGVPRDRTGSGSGTDFTLTISVQPEDLAIVYCHQYLSSRTFGQGTKLEIKR 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 ESGVPRDRTGSGSGTDFTLTISVQPEDLAIVYCHQYLSSRTFGQGTKLEIKR 113

RESULT 3
KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
probe.";
RL Nucleic Acids Res. 13:6531-6544 (1985).
RN [2]
RP SEQUENCE REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBSJ databases.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; X02990; CAA26733.1; -; mRNA.
DR HSSP; P01625; ILVE.
DR SMR; P06314; 21-134.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.

```

```

DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Framework-4.
FT REGION 122 133 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 78.1%; Score 457.5; DB 1; Length 134;
Best Local Similarity 76.3%; Pred. No. 1.0e-39;
Matches 87; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGSLAVPGERVMTMCKSSQSVFFSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
Db 21 DIVMTQSPDLSAVLGRATINCKSSQSVILSSDNKNYLAWYQKPGPRLLIYWASTR 80

Qy 61 ESGVPRDFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
Db 81 ESGVPRDFSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 134

RESULT 4
Q52L64 MOUSE
ID Q52L64 MOUSE PRELIMINARY; PRT; 240 AA.
AC Q52L64;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
TX TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallog D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
TX TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH MGC Project;

```

```

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094049; AAH94049.1; -, mRNA.
DR SMR; Q52L64; 21-240.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26609 MW; CF8630CCC002E52C CRC64;

Query Match 77.2%; Score 452.5; DB 2; Length 240;
Best Local Similarity 75.4%; Pred. No. 1.2e-38;
Matches 86; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EIVLTQSPGSLAVPGERVMTMCKSSQSVFFSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
Db 21 DIVMTQSPDLSAVLGRATINCKSSQSVILSSDNKNYLAWYQKPGPRLLIYWASTR 80

Qy 61 ESGVPRDFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
Db 81 ESGVPRDFSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 134

RESULT 5
Q6KB05 MOUSE
ID Q6KB05 MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SCFV B8E5 protein (Fragment).
GN Names=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -, Other_DNA.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
FT NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 74.0%; Score 433.5; DB 2; Length 255;
Best Local Similarity 76.5%; Pred. No. 1.2e-36;
Matches 88; Conservative 8; Mismatches 14; Indels 5; Gaps 2;

Qy 1 EIVLTQSPGSLAVPGERVMTMCKSSQSVFFSSQKNYLAWYQOIPGQSPRLLIYWASTR 60
Db 137 DIVMTQSPDLSAVLGRATINCKSSQSVILSSDNKNYLAWYQKPGPRLLIYWASTR 196

Qy 61 ESGVPRDFTGSGSGTDTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 112

```

```
Db 197 ESGVDPDRFTGSGGTDFTLTISVQAEDLAVVYCCNDHSHY--PLTFGAGTKLEIK 249
RESULT 6
KV3L HUMAN
ID KV3L HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1094/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; PLO022; K3HUHA.
DR HSSP; P01625; LEEQ.
DR SMR; P18135; 21-129.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 UKL segment.
FT DISULFID 43 109 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 72.5%; Score 425; DB 1; Length 129;
Best Local Similarity 73.7%; Pred. No. 4.1e-36;
Matches 84; Conservative 15; Mismatches 9; Indels 6; Gaps 3;

QY 1 EIVLTQSPGSLAVSPGKRVMTSKSSQSVFFSSQKNYLAWYQQIPGQSPRLIYWASTR 60
Db 21 EIVLTQSPGTLSPGERATLSCASQSV--SSS---YLAWYQKPGQAPRLIYGASSR 75

QY 61 ESGVDPDRFTGSGGTDFTLTISVQAEDLAIYCHQY-LSSRTFGGQTKLEIKR 113
Db 76 ATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGTSPRTFGGQTKVEIKR 129

RESULT 7
```

```
KV40 HUMAN
ID KV40 HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Z00023; CAA77318.1; -; Genomic_DNA.
DR PIR; A01902; K4HU.
DR HSSP; P01625; ILVE.
DR SMR; P06312; 21-121.
DR Ensembl; ENSG00000153586; Homo sapiens.
DR HGNC; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 71.7%; Score 420; DB 1; Length 121;
Best Local Similarity 78.0%; Pred. No. 1.3e-35;
Matches 78; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTSKSSQSVFFSSQKNYLAWYQQIPGQSPRLIYWASTR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPKLLIYWASTR 80

QY 61 ESGVDPDRFTGSGGTDFTLTISVQAEDLAIYCHQYLS 100
Db 81 ESGVDPDRFSGSGGTDFTLTISLSQAEDVAVYCCQYYST 120

RESULT 8
KV3E HUMAN
ID KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
```

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 10-MAY-2005 (Rel. 47, Last annotation update)  
 OS Ig kappa chain V-III region WOL.  
 OC Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa  
 RT group.";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma  
 CC globulin activity.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; A01896; K3HUL.  
 DR HSSP; P01625; 1LVE.  
 DR SMR; P01623; 1-109.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89 By similarity.  
 FT NON TER 109 109  
 SQ SEQUENCE 109 AA; 11746 MW; 566C11586B9CBEE CRC64;  
 Query Match 71.2%; Score 417; DB 1; Length 109;  
 Best Local Similarity 70.2%; Pred. No. 2.3e-35;  
 Matches 80; Conservative 15; Mismatches 13; Indels 6; Gaps 2;  
 QY 1 EIVLTQSPGSLAVPGERVTMCKSQSVFFSSQKKNLAWYQQIPGQSPRLIYWASTR 60  
 DB 1 EIVLTQSPGTLSPGERATLSCRSQSV-----SSGYLGWYQQKPKGAPRLIYGASSR 55  
 QY 61 ESGVPRFTGSGSGTDFTLTISVQPEDLAIIYCHOYLS-SRTFGQGTLEIKR 113  
 DB 56 ATGIPDRFSGSGSGTDFTLTISRLEPDPFAVYCCQYGSIGRTFGGQTKVEIKR 109  
 RESULT 9  
 KV3B HUMAN STANDARD; PRT; 109 AA.  
 ID KV3B HUMAN  
 AC P01620;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-III region SIE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=82046598; PubMed=6794615;  
 RA Andrews D.W., Capra J.D.;  
 RT "Amino acid sequence of the variable regions of light chains from two  
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa

RT group.";  
 RL Biochemistry 20:5816-5822(1981).  
 CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma  
 CC globulin activity.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; A01892; K3HUSI.  
 DR HSSP; P01625; 1LVE.  
 DR SMR; P01620; 1-109.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DISULFID 23 89 By similarity.  
 FT NON TER 109 109  
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3BCD646FFB4 CRC64;  
 Query Match 70.8%; Score 415; DB 1; Length 109;  
 Best Local Similarity 69.3%; Pred. No. 3.7e-35;  
 Matches 79; Conservative 19; Mismatches 10; Indels 6; Gaps 2;  
 QY 1 EIVLTQSPGSLAVPGERVTMCKSQSVFFSSQKKNLAWYQQIPGQSPRLIYWASTR 60  
 DB 1 EIVLTQSPGTLSPGERATLSCRSQSV-----SNSYLAWYQQKPKGAPRLIYGASSR 55  
 QY 61 ESGVPRFTGSGSGTDFTLTISVQPEDLAIIYCHOYLS-SRTFGQGTLEIKR 113  
 DB 56 ATGIPDRFSGSGSGTDFTLTISRLEPDPFAVYCCQYGSIGRTFGGQTKVEIKR 109  
 RESULT 10  
 KV3M HUMAN STANDARD; PRT; 129 AA.  
 ID KV3M HUMAN  
 AC P18136;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-III region HIC precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;  
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Autoantibody-associated kappa light chain variable region gene  
 RT expressed in chronic lymphocytic leukemia with little or no somatic  
 RT mutation. Implications for etiology and immunotherapy.";  
 RL J. Exp. Med. 167:840-852(1988).  
 CC -!- DISEASE: The protein is one of the surface immunoglobulin M  
 CC autoantibodies expressed in patients with chronic lymphocytic  
 CC leukemia.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; P18021; K3HUHI.  
 DR HSSP; P01625; 1EEQ.

```

DR SMR; P18136; 21-129.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HIC.
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 JKI segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;

Query Match 70.6%; Score 414; DB 1; Length 129;
Best Local Similarity 72.8%; Pred. No. 5.7e-35;
Matches 83; Conservative 15; Mismatches 10; Indels 6; Gaps 3;

QY 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSFSSQKNYLAHYQQIPGQSPRLIIYWASTR 60
Db 21 EIVLTQSPGSLSPGERATLSQASQSV--SSS---YLAWYQKPGQAPRLIIYGASSR 75
QY 61 ESGVPRFRFGSGSGTDFTLTISVQPEDLAHYCHQYLSSR-TFGQGTKEIKR 113
Db 76 ATGIPDRFSGSGSGTDFTLTISRLEPDAFYVYQQYSGSPWTFGQGTKEIKR 129

RESULT 11
KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for the
mechanism of antibody production."
RT Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC PIR; A01895; K3HUT1.
DR HSSP; P01625; ILVE.
DR SMR; P01622; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

```

```

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 70.5%; Score 413; DB 1; Length 109;
Best Local Similarity 69.3%; Pred. No. 6e-35;
Matches 79; Conservative 18; Mismatches 11; Indels 6; Gaps 2;

QY 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSFSSQKNYLAHYQQIPGQSPRLIIYWASTR 60
Db 1 EIVLTQSPGSLSPGERATLSQASQSV----SNSFLAWYQKPGQAPRLIIYVASSR 55
QY 61 ESGVPRFRFGSGSGTDFTLTISVQPEDLAHYCHQYLSS-RTFGQGTKEIKR 113
Db 56 ATGIPDRFSGSGSGTDFTLTISRLEPDAFYVYQQYSGSPSTFGQGTKEIKR 109

RESULT 12
Q9UL78_HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1373487;
RA Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
antigen."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1373487;
RA Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
antigen."
RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1552291;
RA Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
RT "Evidence for somatic selection of natural autoantibodies."
RL J. Exp. Med. 175:983-991(1992).
DR EMBL; AF035036; AAD56272.1; -, mRNA.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.

```



[illegible]

```
DR HSSP; P01837; 1KCU.
DR SMR; Q6PIL8; 21-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 69.4%; Score 406.5; DB 2; Length 236;
Best Local Similarity 69.6%; Pred. No. 6.8e-34;
Matches 80; Conservative 18; Mismatches 10; Indels 7; Gaps 3;

QY 1 EIVLTQSPGSLAVSPGERVTMTCKSSQSVFFSSQKNYLAWYQQIPGQSPRLLIYWASTR 60
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 21 ENVLTQSPGTLSPGERATLSCRAQSL--SSS---YLAWYQKPGQAPRLLIYGVSSR 75

QY 61 ESGVPRDFTGSGSGTDFTLTISSVQPEDLAIIYCHQYLSSR--TFGQGTKLEIKR 113
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 76 ATGIPDRFSGSGSGTDFTLTIISRLPEDFAVVYCOQYGSRSPTTFGQGTRLDIKR 130

RESULT 15
KVJG_HUMAN
ID KVJG_HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT "Amino acid sequence of a light chain variable region of a human
rheumatoid factor of the Wa idiotype group, in part predicted by its
reactivity with antipeptide antibodies.";
RL Mol. Immunol. 23:239-244 (1986).
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR PIR; A01893; K3HUGO.
DR HSSP; P01625; 1EK3.
DR SMR; P04206; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
DI SULFID 23 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;
```

```
Query Match 68.9%; Score 404; DB 1; Length 109;
Best Local Similarity 67.5%; Pred. No. 5.1e-34;
Matches 77; Conservative 19; Mismatches 12; Indels 6; Gaps 2;

QY 1 EIVLTQSPGSLAVSPGERVTMTCKSSQSVFFSSQKNYLAWYQQIPGQSPRLLIYWASTR 60
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 EIVLTQSPGTLSPGERATLSCRAA-----LLSRGYLAWYQKPGQAPRLLIYGASSR 55

QY 61 ESGVPRDFTGSGSGTDFTLTISSVQPEDLAIIYCHQYLSS-RTFGQGTKLEIKR 113
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 56 ATGIPDRFSGSGSGTDFTLTIISRLPEDFAVVYCOQYGSRSPTTFGQGTKVEIKR 109

Search completed: May 9, 2006, 01:32:34
Job time : 104.461 secs
```

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:32:56 ; Search time 25.4372 Seconds  
(without alignments)  
367.271 Million cell updates/sec

Title: US-10-700-632-10  
Perfect score: 586  
Sequence: 1 EIVLTQSPGSLAVSPGERVT.....CHQYLSSRTFGQGTKLEIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgm2\_6/ptodata/1/iaa/5\_COMB.pep.\*  
2: /cgm2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgm2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgm2\_6/ptodata/1/iaa/PCUTUS\_COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511	87.2	112	2	US-08-435-516-28
2	499	85.2	113	1	US-08-690-102A-2
3	499	85.2	113	2	US-09-127-902-2
4	499	85.2	113	2	US-09-155-107-2
5	499	85.2	113	4	PCT-US95-09641-2
6	489	83.4	130	2	US-10-146-305-7
7	487	83.1	259	2	US-09-419-788-115
8	485	82.8	112	1	US-07-916-098A-15
9	476	81.2	112	2	US-08-435-516-4
10	476	81.2	113	1	US-08-690-102A-6
11	476	81.2	113	2	US-09-127-902-6
12	476	81.2	113	4	PCT-US93-09641-6
13	476	81.2	113	4	PCT-US93-09641-6
14	476	81.2	301	1	US-08-661-052-14
15	476	81.2	301	2	US-09-188-082-14
16	476	81.2	301	2	US-09-364-088-14
17	476	81.2	301	2	US-09-102-716-14
18	476	81.2	352	2	US-09-203-958A-2
19	476	81.2	553	1	US-08-661-052-16
20	476	81.2	553	2	US-09-188-082-16
21	476	81.2	553	2	US-09-364-088-16
22	476	81.2	553	2	US-09-102-716-16
23	475.5	81.1	113	2	US-08-483-749A-16
24	475.5	81.1	113	4	PCT-US93-08435-4
25	471	80.4	241	1	US-07-916-098A-56
26	467.5	79.8	114	1	US-08-428-257A-76
27	467.5	79.8	114	2	US-07-987-264-16

28	467	79.7	114	2	US-08-929-856-66	Sequence 66, Appl
29	467	79.7	219	1	US-08-353-400-34	Sequence 34, Appl
30	467	79.7	239	1	US-08-353-400-37	Sequence 37, Appl
31	465.5	79.4	113	4	PCT-US93-08435-6	Sequence 6, Appl
32	465.5	79.4	114	2	US-09-025-769B-17	Sequence 17, Appl
33	465.5	79.4	114	2	US-09-490-070A-17	Sequence 17, Appl
34	465.5	79.4	114	2	US-09-490-153-17	Sequence 17, Appl
35	465.5	79.4	114	2	US-09-490-324-17	Sequence 17, Appl
36	464.5	79.3	155	2	US-08-828-741B-11	Sequence 11, Appl
37	464.5	79.3	155	2	US-09-160-567-11	Sequence 11, Appl
38	464.5	79.3	155	2	US-09-710-299-11	Sequence 11, Appl
39	464.5	79.3	155	2	US-09-509-031-11	Sequence 11, Appl
40	464.5	79.3	342	2	US-08-828-741B-6	Sequence 6, Appl
41	464.5	79.3	342	2	US-09-160-567-6	Sequence 6, Appl
42	464.5	79.3	342	2	US-09-710-299-6	Sequence 6, Appl
43	464.5	79.3	342	2	US-09-509-031-6	Sequence 6, Appl
44	464.5	79.3	495	2	US-08-828-741B-4	Sequence 4, Appl
45	464.5	79.3	495	2	US-09-160-567-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-435-516-28  
; Sequence 28, Application US/08435516  
; Patent No. 6500931  
; GENERAL INFORMATION:  
; APPLICANT: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR  
; TITLE OF INVENTION: IMMUNOBLOULIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
; NUMBER OF SEQUENCES: 28  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384  
; FILING DATE: 04-NOV-1992; -02-NOV-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-013  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-08-435-516-28

Query Match 87.2%; Score 511; DB 2; Length 112;  
Best Local Similarity 88.3%; Pred. No. 5.8e-41;  
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy	2	IIVLTQSPGSLAVSPGERVTMTCKSSQSVFSSQKNYLAWYQIQGSPRLIYWASTRE	61
Db	2	IIVLTQSPGSLAVSAGEKVTMTCKSSQSVLYSSQKNYLAWYQIQGSPKLIYWASTRE	61
Qy	62	SGVDPDRFTGSGSTDTLTLTSSVQPEDLAIIYCHQYLSSTFGGQTKLEIK	112
Db	62	SGVDPDRFTGSGSTDTLTLTSSVQABDLAVIYCHQYLSSTFGGQTKLEIK	112

```
RESULT 2
US-08-690-102A-2
; Sequence 2, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-690-102A-2

Query Match 85.2%; Score 499; DB 1; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTCKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
Db 1 DIQLTQSPSSSLAVSAGENVMTCKSSQSVLSANHNKYNLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVPRFTGSGGTDFTLTISVQVEDLAIIYCHQYLSRRTFGGQTKLEIKR 113
Db 61 ESGVPRFTGSGGTDFTLTISRQVEDLAIIYCHQYLSRRTFGGQTKLEIKR 113

RESULT 3
US-09-127-902-2
; Sequence 2, Application US/09127902
; Patent No. 6187287
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA

Query Match 85.2%; Score 499; DB 2; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTCKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
Db 1 DIQLTQSPSSSLAVSAGENVMTCKSSQSVLSANHNKYNLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVPRFTGSGGTDFTLTISVQVEDLAIIYCHQYLSRRTFGGQTKLEIKR 113
Db 61 ESGVPRFTGSGGTDFTLTISRQVEDLAIIYCHQYLSRRTFGGQTKLEIKR 113

RESULT 4
US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
; US-09-155-107-2

Query Match 85.2%; Score 499; DB 2; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTCKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
```

```
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,902
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,102
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-127-902-2

Query Match 85.2%; Score 499; DB 2; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTCKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
Db 1 DIQLTQSPSSSLAVSAGENVMTCKSSQSVLSANHNKYNLAWYQQKPGQSPKLLIYWASTR 60
QY 61 ESGVPRFTGSGGTDFTLTISVQVEDLAIIYCHQYLSRRTFGGQTKLEIKR 113
Db 61 ESGVPRFTGSGGTDFTLTISRQVEDLAIIYCHQYLSRRTFGGQTKLEIKR 113

RESULT 4
US-09-155-107-2
; Sequence 2, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
; US-09-155-107-2

Query Match 85.2%; Score 499; DB 2; Length 113;
Best Local Similarity 85.8%; Pred. No. 7.9e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPGSLAVSPGKRVMTCKSSQSVFFSSQKYNLAWYQQIPGQSPRLIIYWASTR 60
```

Db 1 DIQLTSPSLAVSAGENVMTMCKSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
 QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRTFGGKLEIKR 113  
 Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRTFGGKLEIKR 113

RESULT 5  
 PCT-US95-09641-2  
 ; Sequence 2, Application PC/TUS9509641  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED  
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS  
 ; NUMBER OF SEQUENCES: 21  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/09641  
 ; FILING DATE: 11-AUG-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/289,576  
 ; FILING DATE: 12-AUG-1994  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 113 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US95-09641-2

Query Match 85.2%; Score 499; DB 4; Length 113;  
 Best Local Similarity 85.8%; Pred. No. 7.9e-40;  
 Matches 97; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAIIYCHQVLSRTFGGKLEIKR 60  
 Db 1 DIQLTSPSLAVSAGENVMTMCKSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
 QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRTFGGKLEIKR 113  
 Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRTFGGKLEIKR 113

RESULT 6  
 US-10-146-305-7  
 ; Sequence 7, Application US/10146305  
 ; Patent No. 6939956  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YUHAN CORPORATION  
 ; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV  
 ; TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME  
 ; FILE REFERENCE: OV17440  
 ; CURRENT APPLICATION NUMBER: US/10/146,305  
 ; CURRENT FILING DATE: 2002-05-15  
 ; PRIOR APPLICATION NUMBER: KR 10-2001-26634  
 ; PRIOR FILING DATE: 2001-05-16  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: Kopatentin 1.71  
 ; SEQ ID NO 7  
 ; LENGTH: 130  
 ; TYPE: PRT  
 ; ORGANISM: Escherichia coli  
 ; US-10-146-305-7

Query Match 83.4%; Score 489; DB 2; Length 130;  
 Best Local Similarity 82.3%; Pred. No. 8e-39;  
 Matches 93; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAIIYCHQVLSRTFGGKLEIKR 60  
 Db 1 DIVMSQSPSLAVSAGENVMTMCKSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 60  
 QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRTFGGKLEIKR 113  
 Db 61 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRTFGGKLEIKR 113

RESULT 7  
 US-09-419-788-115  
 ; Sequence 115, Application US/09419788  
 ; Patent No. 6825325  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FISCHER, Rainer  
 ; APPLICANT: SCHILLBERG, Stefan  
 ; APPLICANT: NAHRING, Jorg  
 ; APPLICANT: SACK, Markus  
 ; APPLICANT: MONECKE, Michael  
 ; APPLICANT: LIAO, Yu-Cai  
 ; APPLICANT: SPIEGEL, Holger  
 ; APPLICANT: ZIMMERMAN, Sabine  
 ; APPLICANT: EMANS, Neil  
 ; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease  
 ; TITLE OF INVENTION: Resistance  
 ; FILE REFERENCE: 0147-0189P  
 ; CURRENT APPLICATION NUMBER: US/09/419,788  
 ; CURRENT FILING DATE: 1999-10-18  
 ; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP  
 ; EARLIER FILING DATE: 1998-10-16  
 ; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA  
 ; EARLIER FILING DATE: 1998-10-16  
 ; NUMBER OF SEQ ID NOS: 163  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 115  
 ; LENGTH: 259  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no  
 ; OTHER INFORMATION: natural origin  
 ; US-09-419-788-115

Query Match 83.1%; Score 487; DB 2; Length 259;  
 Best Local Similarity 82.3%; Pred. No. 2.6e-38;  
 Matches 93; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAIIYCHQVLSRTFGGKLEIKR 60  
 Db 141 DIVLSQSPSLAVSAGENVMTMCKSSQSVLYSANHKNYLAWYQKQSPKLLIYWASTR 200  
 QY 61 ESGVDRFTGSGGTDFTLTISVQPEDLAIIYCHQVLSRTFGGKLEIKR 113  
 Db 201 ESGVDRFTGSGGTDFTLTISRQVEDLAIIYCHQVLSRTFGGKLEIKR 253

RESULT 8  
 US-07-916-098A-15  
 ; Sequence 15, Application US/07916098A  
 ; Patent No. 5871732  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURKLY, LINDA C.  
 ; APPLICANT: CHISHOLM, PATRICIA L.  
 ; APPLICANT: THOMAS, DAVID W.  
 ; APPLICANT: ROSA, MARGARET D.  
 ; APPLICANT: ROSA, JOSEPH J.  
 ; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
 ; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
 ; NUMBER OF SEQUENCES: 61  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
 ; STREET: 10 SOUTH WACKER DRIVE  
 ; CITY: CHICAGO



RESULT 12  
US-09-155-107-6  
; Sequence 6, Application US/09155107  
; Patent No. 6254868

		Query Match	81.2%;	Score 476;	DB 4;	Length 113;
		Best Local Similarity	78.8%;	Pred. No. 1.2e-37;		
		Matches	89;	Conservative 12;	Mismatches 12;	Indels 0; Gaps 0;
Qy	1	EIVLTQSGSLVAPGERTVMCKSSQSQSVFFSSQKNYLAWYQOIFQCSPRLLIYNASTR	60			
	:	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
Dd	1	DIQLTQPSLSASVGDRVTMSCKSSQSQSVLYSANHKNYLAWYQKPGKAPKLIIYNASTR	60			
Qy	61	EGGVDPRTFGSSGGDTFTITISVSQPEDIAIYYCHOYLSRRPFGQTGLEIKR	113			
Dd	61	EGGVSPRFSGSGSGDTFTITISLOPEDATYYCHOYLSWSWTFGGGTGLEIKR	113			

## RESULT 14

US-08-661-052-14  
; Sequence 14, Application US/08661052  
; Patent No. 5837243  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano  
; APPLICANT: Chezia Somasundaram  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
; OF ANTI-FC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,052  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,172  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-043CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 301 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-661-052-14

Query Match 81.2%; Score 476; DB 1; Length 301;  
Best Local Similarity 78.6%; Pred. No. 3.3e-37;  
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;  
  
QY 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSQKNYLAWYQOIIPGQSPRLLIYWASTR 60  
DB 155 DIQLTQSPSSLASVGDRTVITCKSSQSVLYSSNQKNYLAWYQKPGKAPKLLIYWASTR 214  
  
QY 61 ESGVDPRTGSGSGTDFTLTISVQPEDLAIIYCHQYLSRRTFGQGTKEIK 112  
DB 215 ESGVPSRFSGSGGTDFTTISLQPEDIAITYYCHQYLSSTWTFGQGTKEIK 266

## RESULT 15

US-09-188-082-14  
; Sequence 14, Application US/09188082  
; Patent No. 6270765  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano  
; APPLICANT: Chezia Somasundaram  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
; OF ANTI-FC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510

; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/188,082  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/661,052  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-043CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 301 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-188-082-14  
  
Query Match 81.2%; Score 476; DB 2; Length 301;  
Best Local Similarity 78.6%; Pred. No. 3.3e-37;  
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;  
  
QY 1 EIVLTQSPGSLAVSPGERVTMSCKSSQSVFFSSQKNYLAWYQOIIPGQSPRLLIYWASTR 60  
DB 155 DIQLTQSPSSLASVGDRTVITCKSSQSVLYSSNQKNYLAWYQKPGKAPKLLIYWASTR 214  
  
QY 61 ESGVDPRTGSGSGTDFTLTISVQPEDLAIIYCHQYLSRRTFGQGTKEIK 112  
DB 215 ESGVPSRFSGSGGTDFTTISLQPEDIAITYYCHQYLSSTWTFGQGTKEIK 266  
  
Search completed: May 9, 2006, 01:35:39  
Job time : 26.4372 secs



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:57:07 ; Search time 84.8723 Seconds  
(without alignments)  
556.303 Million cell updates/sec

Title: US-10-700-632-10  
Perfect score: 586  
Sequence: 1 EIVLTSPGSLAVSPGERVT.....CHOYLSRRTFGQTKLEIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*\*
- 2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep:\*\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US10B\_PUBCOMB.pep:\*\*
- 6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	100.0	113	5	US-10-700-632-10
2	543	92.7	113	5	US-10-700-632-8
3	543	92.7	114	5	US-10-700-632-62
4	511	87.2	112	4	US-10-229-335-28
5	510	87.0	113	5	US-10-722-849-4
6	510	87.0	113	6	US-11-004-659-4
7	510	87.0	133	5	US-10-723-003-10
8	510	87.0	133	6	US-11-004-639-10
9	510	87.0	239	5	US-10-723-003-14
10	510	87.0	239	6	US-11-004-639-14
11	510	87.0	661	5	US-10-723-003-34
12	510	87.0	661	6	US-11-004-639-34
13	509	86.9	112	4	US-10-056-052-10
14	509	86.9	112	5	US-10-816-938-31
15	508	86.7	112	4	US-10-056-052-6
16	507	86.5	112	4	US-10-056-052-18
17	503	85.8	112	4	US-10-056-052-14
18	499	85.2	113	3	US-09-741-843-2
19	499	85.2	113	3	US-09-894-839-2
20	499	85.2	113	3	US-09-988-013A-2
21	499	85.2	113	4	US-10-446-689-2
22	499	85.2	113	5	US-10-787-378-2
23	499	85.2	113	5	US-10-974-678-2
24	499	85.2	272	4	US-10-207-655-14
25	499	85.2	272	4	US-10-053-530-14
26	499	85.2	272	6	US-11-089-511-14
27	499	85.2	272	6	US-11-089-190-14

28	499	85.2	272	6	US-11-088-570-14	Sequence 14, Appl
29	499	85.2	272	6	US-11-088-737-14	Sequence 14, Appl
30	499	85.2	272	6	US-11-088-569-14	Sequence 14, Appl
31	499	85.2	272	6	US-11-088-693-14	Sequence 14, Appl
32	499	85.2	272	6	US-11-089-367-14	Sequence 14, Appl
33	499	85.2	272	6	US-11-089-368-14	Sequence 14, Appl
34	497	84.8	132	6	US-11-013-537-2	Sequence 2, Appl
35	497	84.8	132	6	US-11-013-537-1	Sequence 1, Appl
36	489	83.4	130	4	US-10-146-305-7	Sequence 7, Appl
37	478	81.6	238	4	US-10-467-253-14	Sequence 14, Appl
38	477.5	81.5	146	5	US-10-830-899-56	Sequence 56, Appl
39	477.5	81.5	146	5	US-10-830-899-63	Sequence 63, Appl
40	477.5	81.5	146	5	US-10-861-662-56	Sequence 56, Appl
41	477.5	81.5	146	5	US-10-861-662-63	Sequence 63, Appl
42	476	81.2	112	4	US-10-229-335-4	Sequence 4, Appl
43	476	81.2	352	3	US-09-203-958A-2	Sequence 2, Appl
44	476	81.2	352	5	US-10-764-131-2	Sequence 2, Appl
45	473	80.7	112	4	US-10-467-253-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-10-700-632-10

; Sequence 10, Application US/10700632

; Publication No. US20050118183A1

; GENERAL INFORMATION:

; APPLICANT: ImmunoGen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

; FILE REFERENCE: A8427

; CURRENT APPLICATION NUMBER: US/10/700,632

; CURRENT FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/424,332

; PRIOR FILING DATE: 2002-11-07

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Humanized My9-6 antibody light chain variable region

US-10-700-632-10

Query Match	100.0%;	Score 586;	DB 5;	Length 113;
Best Local Similarity	100.0%;	Pred. No. 5.1e-43;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTSPGSLAVSPGERVTMTCKSSQSVFFSSQKNYLAWYQOI PQSPRLLIYWASTR	60	
Db	1	EIVLTSPGSLAVSPGERVTMTCKSSQSVFFSSQKNYLAWYQOI PQSPRLLIYWASTR	60	
QY	61	ESGVDPRTFGSGSGDFTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR	113	
Db	61	ESGVDPRTFGSGSGDFTLTITSSVQPEDLAIIYCHQYLSRRTFGQTKLEIKR	113	

RESULT 2

US-10-700-632-8

; Sequence 8, Application US/10700632

; Publication No. US20050118183A1

; GENERAL INFORMATION:

; APPLICANT: ImmunoGen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

; FILE REFERENCE: A8427

; CURRENT APPLICATION NUMBER: US/10/700,632

; CURRENT FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/424,332

; PRIOR FILING DATE: 2002-11-07

; NUMBER OF SEQ ID NOS: 94

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-8

Query Match      92.7%; Score 543; DB 5; Length 113;
Best Local Similarity 93.8%; Pred. No. 2.6e-39;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
Db 2 IVLTQSPSSSLAVSAGEKVTMCKSSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTRE 61

QY 62 SGVPRFTGSGSGTDTFTLTSSVQPEDLAIIYCHQYLSSRTFGGQTKLEIKR 113
Db 62 SGVPRFTGSGSGTDTFTLTSSVQSEDLAIIYCHQYLSSRTFGGQTKLEIKR 113

RESULT 3
US-10-700-632-62
; Sequence 62, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-62

Query Match      92.7%; Score 543; DB 5; Length 114;
Best Local Similarity 93.8%; Pred. No. 2.6e-39;
Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
Db 2 IVLTQSPSSSLAVSAGEKVTMCKSSQSVFFSSQKNYLAWYQIQGSPKLLIYWASTRE 61

QY 62 SGVPRFTGSGSGTDTFTLTSSVQPEDLAIIYCHQYLSSRTFGGQTKLEIKR 113
Db 62 SGVPRFTGSGSGTDTFTLTSSVQSEDLAIIYCHQYLSSRTFGGQTKLEIKR 113

RESULT 4
US-10-229-335-28
; Sequence 28, Application US/10229335
; Publication No. US20030144483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/229,335
; FILING DATE: 26-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match      87.2%; Score 511; DB 4; Length 112;
Best Local Similarity 88.3%; Pred. No. 1.5e-36;
Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
Db 2 IVMTQSPSSSLAVSAGEKVTMCKSSQSVLYSSQKNYLAWYQIQGSPKLLIYWASTRE 61

QY 62 SGVPRFTGSGSGTDTFTLTSSVQPEDLAIIYCHQYLSSRTFGGQTKLEIKR 112
Db 62 SGVPRFTGSGSGTDTFTLTSSVQAEADLAIIYCHQYLSSRTFGGQTKLEIKR 112

RESULT 5
US-10-722-849-4
; Sequence 4, Application US/10722849
; Publication No. US20050031617A1
; GENERAL INFORMATION:
; APPLICANT: WA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR CANCER
; FILE REFERENCE: 549062000100
; CURRENT APPLICATION NUMBER: US/10/722,849
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 03129123.6
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-722-849-4

Query Match      87.0%; Score 510; DB 5; Length 113;
Best Local Similarity 86.6%; Pred. No. 1.8e-36;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIYWASTRE 61
Db 2 IVMTQSPSSSLAVSAGEKVTMCKSSQSVLYSSQKNYLAWYQIQGSPKLLIYWASTRE 61

QY 62 SGVPRFTGSGSGTDTFTLTSSVQAEADLAIIYCHQYLSSRTFGGQTKLEIKR 113
Db 62 SGVPRFTGSGSGTDTFTLTSSVQAEADLAIIYCHQYFSSYTFGGGQTKLEIKR 113

RESULT 6
```



```
QY 62 SGVPRFTGSGGTDFTLTISVQPEDLAIVYCHOYLSRRTFGQGTKEIKR 113
Db 82 SGVPRFTGSGGTDFTLTISVQABDLAVYVYCHQYFSSYTFGGGTKEIKR 133

RESULT 10
US-11-004-639-14
; Sequence 14, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-14

Query Match 87.0%; Score 510; DB 6; Length 239;
Best Local Similarity 86.6%; Pred. No. 3.8e-36;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIIYWASTRE 61
Db 22 IMMTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQIQGSPKLLIYWASTRE 81

QY 62 SGVPRFTGSGGTDFTLTISVQPEDLAIVYCHOYLSRRTFGQGTKEIKR 113
Db 82 SGVPRFTGSGGTDFTLTISVQABDLAVYVYCHQYFSSYTFGGGTKEIKR 133

RESULT 11
US-10-723-003-34
; Sequence 34, Application US/107233003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-723-003-34

Query Match 87.0%; Score 510; DB 5; Length 661;
```

```
Best Local Similarity 86.6%; Pred. No. 1e-35;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIIYWASTRE 61
Db 550 IMMTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQIQGSPKLLIYWASTRE 609

QY 62 SGVPRFTGSGGTDFTLTISVQPEDLAIVYCHOYLSRRTFGQGTKEIKR 113
Db 610 SGVPRFTGSGGTDFTLTISVQABDLAVYVYCHQYFSSYTFGGGTKEIKR 661

RESULT 12
US-11-004-639-34
; Sequence 34, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 549062000200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/723,003
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: CN 2003101199300
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: CN 031292909
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-004-639-34

Query Match 87.0%; Score 510; DB 6; Length 661;
Best Local Similarity 86.6%; Pred. No. 1e-35;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFFSSQKNYLAWYQIQGSPRLIIYWASTRE 61
Db 550 IMMTQSPSLAVSAGEKVTMCKSSQSVLYSSNQKNYLAWYQIQGSPKLLIYWASTRE 609

QY 62 SGVPRFTGSGGTDFTLTISVQPEDLAIVYCHOYLSRRTFGQGTKEIKR 113
Db 610 SGVPRFTGSGGTDFTLTISVQABDLAVYVYCHQYFSSYTFGGGTKEIKR 661

RESULT 13
US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLPA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
```

; PRIOR APPLICATION NUMBER: 60/264,072  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-056-052-10

Query Match 86.9%; Score 509; DB 4; Length 112;  
Best Local Similarity 87.4%; Pred. No. 2.2e-36;  
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
QY 2 IVLTQSPGSLAVSPGGERVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPRLIIYWASTRE 61  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 IMVTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGSPKLLIYWASTRE 61  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 62 SGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLSSTRTFGQGTKEIK 112  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 62 SGVPDRFTGSGGTDFTLTISVQAEADLAVYCHQYLSSTRTFGGQGTKEIK 112  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

## RESULT 14

US-10-816-938-31  
; Sequence 31, Application US/10816938  
; Publication No. US20040229301A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Baiyang  
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof  
; FILE REFERENCE: 1861.1670002  
; CURRENT APPLICATION NUMBER: US/10/816,938  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 31  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-816-938-31

Query Match 86.9%; Score 509; DB 5; Length 112;  
Best Local Similarity 87.4%; Pred. No. 2.2e-36;  
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
QY 2 IVLTQSPGSLAVSPGGERVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPRLIIYWASTRE 61  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 IMVTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGSPKLLIYWASTRE 61  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 62 SGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLSSTRTFGQGTKEIK 112  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 62 SGVPDRFTGSGGTDFTLTISVQAEADLAVYCHQYLSSTRTFGGQGTKEIK 112  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

## RESULT 15

US-10-056-052-6  
; Sequence 6, Application US/10056052  
; Publication No. US20030099656A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M  
; APPLICANT: HUTCHINS, Jeff T  
; APPLICANT: DOMANSKI, Paul  
; APPLICANT: PATEL, Pratiksha  
; APPLICANT: HALL, Andrea  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .  
; FILE REFERENCE: P07069US04/BAS  
; CURRENT APPLICATION NUMBER: US/10/056,052  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/308,116  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/298,413  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/274,611

; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: 60/264,072  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-056-052-6  
Query Match 86.7%; Score 508; DB 4; Length 112;  
Best Local Similarity 86.5%; Pred. No. 2.7e-36;  
Matches 96; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
QY 2 IVLTQSPGSLAVSPGGERVTMSCKSSQSVFFSSQKNYLAWYQQIPGQSPRLIIYWASTRE 61  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 2 IMVTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGSPKLLIYWASTRE 61  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 62 SGVPDRFTGSGGTDFTLTISVQPEDLAIIYCHQYLSSTRTFGQGTKEIK 112  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 62 SGVPDRFTGSGGTDFTLTISVQAEADLAVYCHQYLSSTRTFGGQGTKEIK 112  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: May 9, 2006, 02:04:57  
Job time : 85.8723 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2006, 01:59:22 ; Search time 13.4524 Seconds  
(without alignments)  
388.792 Million cell updates/sec

Title: US-10-700-632-10  
Perfect score: 586  
Sequence: 1 EIVLTQSPGSLAVSPGERVT.....CHOYLSRRTFGQGTLEIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:  
1: /SIDSS5/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /SIDSS5/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /SIDSS5/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /SIDSS5/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /SIDSS5/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
7: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
8: /SIDSS5/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
9: /SIDSS5/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
10: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
11: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
12: /SIDSS5/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	516	88.1	116	9	US-10-981-356A-1
2	516	88.1	116	11	US-11-096-046-1
3	516	88.1	116	9	US-10-981-356A-29
4	516	88.1	667	11	US-11-096-046-29
5	509	86.9	112	11	US-11-136-559-10
6	508	86.7	112	11	US-11-136-559-6
7	507	86.5	112	11	US-11-136-559-18
8	503	85.8	112	11	US-11-136-559-14
9	496	84.6	112	11	US-11-136-559-22
10	481.5	82.2	259	9	US-10-512-184-31
11	481.5	82.2	329	9	US-10-512-184-68
12	476	81.2	116	9	US-10-981-356A-3
13	476	81.2	116	11	US-11-096-046-3
14	476	81.2	666	9	US-10-981-356A-25
15	476	81.2	666	9	US-10-981-356A-27
16	476	81.2	666	9	US-10-981-356A-28
17	476	81.2	666	11	US-11-096-046-27
18	476	81.2	667	11	US-11-096-046-25
19	476	81.2	667	11	US-11-096-046-28
20	476	81.2	692	9	US-10-981-356A-26
21	476	81.2	695	11	US-11-096-046-26

22	473.5	80.8	114	11	US-11-127-677-27	Sequence 27, Appl
23	469.5	80.1	259	9	US-10-512-184-33	Sequence 33, Appl
24	469.5	80.1	329	9	US-10-512-184-70	Sequence 70, Appl
25	465.5	79.4	114	9	US-10-834-397-17	Sequence 17, Appl
26	463	79.0	115	9	US-10-771-257-27	Sequence 27, Appl
27	460.5	78.6	113	10	US-11-219-563-71	Sequence 71, Appl
28	460.5	78.6	113	10	US-11-219-563-91	Sequence 91, Appl
29	460.5	78.6	113	11	US-11-218-813-71	Sequence 71, Appl
30	460.5	78.6	113	11	US-11-218-813-91	Sequence 91, Appl
31	460	78.5	133	8	US-10-511-937-2965	Sequence 2965, Ap
32	457.5	78.1	115	9	US-10-834-397-31	Sequence 31, Appl
33	457.5	78.1	115	9	US-10-834-397-49	Sequence 49, Appl
34	456.5	77.9	114	9	US-10-530-171-8	Sequence 8, Appl
35	456.5	77.9	135	11	US-11-158-505-35	Sequence 35, Appl
36	453	77.3	666	9	US-10-981-356A-30	Sequence 30, Appl
37	453	77.3	667	11	US-11-096-046-30	Sequence 30, Appl
38	449.5	76.7	259	9	US-10-512-184-34	Sequence 34, Appl
39	449.5	76.7	371	9	US-10-512-184-71	Sequence 71, Appl
40	449.5	76.7	626	9	US-10-512-184-49	Sequence 49, Appl
41	448.5	76.5	114	9	US-10-771-257-72	Sequence 72, Appl
42	448.5	76.5	114	11	US-11-127-677-70	Sequence 70, Appl
43	448.5	76.5	678	11	US-11-202-507A-11	Sequence 11, Appl
44	448.5	76.5	679	11	US-11-202-507A-5	Sequence 5, Appl
45	444.5	75.9	118	10	US-11-075-891-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-10-981-356A-1  
; Sequence 1, Application US/10981356A  
; Publication No. US20060015952A1  
; GENERAL INFORMATION:  
; APPLICANT: FILVAROFF, ELLEN H.  
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT  
; FILE REFERENCE: P2068R1  
; CURRENT APPLICATION NUMBER: US/10/981,356A  
; PRIOR FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: US 60/520,398  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/557,951  
; PRIOR FILING DATE: 2004-03-31  
; NUMBER OF SEQ ID NOS: 45  
; SEQ ID NO 1  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-10-981-356A-1

Query Match	88.1%	Score 516;	DB 9;	Length 116;
Best Local Similarity	86.7%	Pred. No. 8.2e-31;		
Matches	98;	Conservative	8;	Mismatches 7; Indels 0; Gaps 0;
Qy	1	EIVLTQSPGSLAVSPGERVTMCKSQSVFFSSQKXNYLAWYQQIPGQSPRLIYWASTR	60	
Db	1	DIMWTQSPSLAVSAGEKVTMCKSQSVLYSSQKXNYLAWYQQKPGQSPKLLIYWASTR	60	
Qy	61	ESGVPRFTGSGSGTFTLTISVQPEDLAIVYCHQYLSRRTFGQGTLEIKR	113	
Db	61	ESGVPRFTGSGSGTFTLTISVQAEADLAVYCHQYLSRSDTFGGQGTLEIKR	113	

RESULT 2  
US-11-096-046-1  
; Sequence 1, Application US/11096046  
; Publication No. US20050276802A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, CAMELLIA W.  
; APPLICANT: FERRARA, NAPOLEONE  
; APPLICANT: FILVAROFF, ELLEN H.  
; APPLICANT: MAO, WEIGUANG  
; APPLICANT: PRESTA, LEONARD G.





Qy 62 SGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112  
Db 62 SGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112

## RESULT 6

US-11-136-559-6  
; Sequence 6, Application US/11136559  
; Publication No. US20050287164A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M  
; APPLICANT: HUTCHINS, Jeff T  
; APPLICANT: DOMANSKI, Paul  
; APPLICANT: PATEL, Pratiksha  
; APPLICANT: HALL, Andrea  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .  
; FILE REFERENCE: P07069US04/BAS  
; CURRENT APPLICATION NUMBER: US/11/136,559  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/056,052  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/308,116  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/298,413  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/274,611  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: 60/264,072  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-136-559-6

Query Match 86.7%; Score 508; DB 11; Length 112;  
Best Local Similarity 86.5%; Pred. No. 3e-30;  
Matches 96; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
Qy 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAIVYCHQYLSRRTFGGQTKLEIK 112  
Db 2 IMVTQSPSSLAIVSAGEKVTMCKSSQSVLYSSNQKNYLAIVYCHQYLSRRTFGGQTKLEIK 112  
Qy 62 SGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112  
Db 62 SGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112

## RESULT 7

US-11-136-559-18  
; Sequence 18, Application US/11136559  
; Publication No. US20050287164A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M  
; APPLICANT: HUTCHINS, Jeff T  
; APPLICANT: DOMANSKI, Paul  
; APPLICANT: PATEL, Pratiksha  
; APPLICANT: HALL, Andrea  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .  
; FILE REFERENCE: P07069US04/BAS  
; CURRENT APPLICATION NUMBER: US/11/136,559  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/056,052  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/308,116  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/298,413  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/274,611  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: 60/264,072

; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-136-559-18  
Query Match 86.5%; Score 507; DB 11; Length 112;  
Best Local Similarity 86.6%; Pred. No. 3.5e-30;  
Matches 97; Conservative 8; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 EIVLTQSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAIVYCHQYLSRRTFGGQTKLEIK 112  
Db 1 DIVMTQSPDLSAVSLGERVTMCKSSQSVLYSSNQKNYLAIVYCHQYLSRRTFGGQTKLEIK 112  
Qy 61 ESGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112  
Db 61 ESGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112

## RESULT 8

US-11-136-559-14  
; Sequence 14, Application US/11136559  
; Publication No. US20050287164A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M  
; APPLICANT: HUTCHINS, Jeff T  
; APPLICANT: DOMANSKI, Paul  
; APPLICANT: PATEL, Pratiksha  
; APPLICANT: HALL, Andrea  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .  
; FILE REFERENCE: P07069US04/BAS  
; CURRENT APPLICATION NUMBER: US/11/136,559  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/056,052  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/308,116  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/298,413  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/274,611  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: 60/264,072  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-136-559-14  
Query Match 85.8%; Score 503; DB 11; Length 112;  
Best Local Similarity 86.5%; Pred. No. 6.8e-30;  
Matches 96; Conservative 7; Mismatches 8; Indels 0; Gaps 0;  
Qy 2 IVLTQSPGSLAVSPGERVTMCKSSQSVFSSQKNYLAIVYCHQYLSRRTFGGQTKLEIK 112  
Db 2 IMVTQSPSSLAIVSAGEKVTMCKSSQSVLYSSNQKNYLAIVYCHQYLSRRTFGGQTKLEIK 112  
Qy 62 SGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112  
Db 62 SGVDPDRFTGSGGDTFTLTISVQPEDLAIVYCHQYLSRRTFGGQTKLEIK 112

RESULT 9  
US-11-136-559-22  
; Sequence 22, Application US/11136559  
; Publication No. US20050287164A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M

```

; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; OTHER INFORMATION: Staphylococcus aureus
US-11-136-559-22

Query Match      84.6%; Score 496; DB 11; Length 112;
Best Local Similarity 85.6%; Pred. No. 2.2e-29;
Matches 95; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 2 IVLTPSGSLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLIIYWASTRE 61
Db 2 IMTTPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGQSPKLLIYWASTRE 61

QY 62 SGVPDRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 112
Db 62 SGVPDRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 112

RESULT 10
US-10-512-184-31
; Sequence 31, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VDCw with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

Query Match      82.2%; Score 481.5; DB 9; Length 259;
Best Local Similarity 82.5%; Pred. No. 4.5e-28;
Matches 94; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 EIVLTQPSGLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLIIYWASTR 60
Db 138 DIVLSQSPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGQSPKLLIYWASTR 197

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113

```

```

Db 198 ESGVPDRFTGSGGTDFTLTITSSVKAEDLAVYCOQYISYPTFGSGTKLEIKR 251

RESULT 11
US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

Query Match      82.2%; Score 481.5; DB 9; Length 329;
Best Local Similarity 82.5%; Pred. No. 5.4e-28;
Matches 94; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 EIVLTQPSGLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLIIYWASTR 60
Db 208 DIVLSQSPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGQSPKLLIYWASTR 267

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
Db 268 ESGVPDRFTGSGGTDFTLTITSSVKAEDLAVYCOQYISYPTFGSGTKLEIKR 321

RESULT 12
US-10-981-356A-3
; Sequence 3, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-3

Query Match      81.2%; Score 476; DB 9; Length 116;
Best Local Similarity 77.0%; Pred. No. 6e-28;
Matches 87; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQPSGLAVSPGERVTMCKSSQSVFPSSQKNYLAWYQOIPGQSPRLIIYWASTR 60
Db 1 DQMTQSPSSSLAVSAGEKVTMCKSSQSVLYSNQKNYLAWYQOKPGQSPKLLIYWASTR 60

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQPEDLAIIYCHQYLS-SRTFGQGTKEIKR 113

```

```

RESULT 13
US-11-096-046-3
; Sequence 3, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096.046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-3

Query Watch      81.2%; Score 476; DB 11; Length 116;
Best Local Similarity 77.0%; Pred. No. 6e-28;
Matches 87; Conservative 16; Mismatches 10; Indels 0; Gaps 0

QY   1 EIVLTQPGSLVSPGERTVTKCSKSSGVPSFSSOKNYLAWYQQIQGPSRLLIYWASTR 60
    :|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db   1 DLIQTQSPSSLASVGVDRTITCRASQSVLYSSNQKNYLAWYQQKPKAPKLLIYWASTR 60
    :|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||

QY   61 ESGVPDRFTGGSGGDTFLTITSISSQVEDLAIIYCHOYLSRSRTFGQGTKLEIKR 113
    :|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db   61 ESGVPSRFGSGSGTDFLTITSISSLPQEDPATYICHVOYLSSDTFGQGTKEIKR 113
    :|:|||||:|:|:|||||:~::~|||:~::~|||:~::~|||:~::~|||:~::~|||

RESULT 14

```

## RESULT 14

**THIS PAGE BLANK (USPTO)**